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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 6-17-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 091915,814
Location (Bldg/Room#): 2028 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: A S Model to H S L Eps.

Inventors (please provide full names): Butler et al.

Earliest Priority Date: 7/26/01

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Seq ID No: 3

- Between NTS 1 - 970 only.
- Score over length
- 70% homology limit
- Size range 8- 50 NTS.

No interference please.

Thanks.

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Type of Search

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Searcher: _____

NA Sequence (#)

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OM nucleic - nucleic search, using sw model

Run on: June 27, 2005, 16:56:58 ; Search time 8 Seconds

(without alignments)
3.735 Million cell updates/sec

Title: us-09-915-814-3
Perfect score: 970

Sequence: 1 ctctctgttaagagatgtcta.....tttctggatgggtcgccat 970

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 830 seqs, 15403 residues

Total number of hits satisfying chosen parameters:

1660

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 838 summaries
rungdb: *

Database :

Query %

Match Length DB ID

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2.2	2.3	31	1 AA129665	Human single nucle
c	2	21.6	2.2	29 1 AA04056	Polymorphic fragme
c	3	20	2.1	20 1 AB282630	Human HSL chimeric
c	4	20	2.1	20 1 AB282640	Human HSL chimeric
c	5	20	2.1	20 1 AB282631	Human HSL chimeric
c	6	20	2.1	20 1 AB282643	Human HSL chimeric
c	7	20	2.1	20 1 AB282633	Human HSL chimeric
c	8	20	2.1	20 1 AB282638	Human HSL chimeric
c	9	20	2.1	20 1 AB282635	Human HSL chimeric
c	10	20	2.1	20 1 AB282637	Human HSL chimeric
c	11	20	2.1	20 1 AB282639	Human HSL chimeric
c	12	20	2.1	20 1 AB282634	Human HSL chimeric
c	13	20	2.1	20 1 AB282632	Human HSL chimeric
c	14	20	2.1	20 1 AB282636	Human HSL chimeric
c	15	20	2.1	20 1 AB282641	Human HSL chimeric
c	16	20	2.1	20 1 AB282642	Human HSL chimeric
c	17	18.8	1.9	26 1 ADD01367	Human TCH039 codin
c	18	18.6	1.9	25 1 ACK19838	Human microarray D
c	19	18.4	1.9	24 1 ADD057923	M. tuberculosis Rv
c	20	18.2	1.9	24 1 AAT94895	Human G protein co
c	21	18.2	1.9	25 1 ABN12495	Human GDMLP-1 25-m
c	22	18.2	1.9	25 1 ABN12494	Human GDMLP-1 25-m
c	23	18.2	1.9	25 1 ABN12494	Human GDMLP-1 25-m
c	24	18.2	1.9	25 1 ACN75585	Human GDMLP-1 prob
c	25	18.2	1.9	25 1 ACN75584	Human GDMLP-1 prob
c	26	18.2	1.9	25 1 ACN75583	Human GDMLP-1 prob
c	27	17.8	1.8	25 1 ACK19737	Human microarray D
c	28	17.6	1.8	25 1 ACH58052	DNA target sequenc
c	29	17.4	1.8	20 1 AAT11438	Retinoblastoma Gen
c	30	17	1.8	20 1 AA269909	Human biallelic ma
c	31	16.8	1.7	20 1 AA96514	Primer used to amp
c	32	16.8	1.7	20 1 ADT179687	Mouse HMG-CoA redu
c	33	16.8	1.7	20 1 ADT179880	Mouse HMG-CoA redu

34	c 35	16.8	16.6	1.7	ACCC70796
	c 36	16.6	1.7	22	AAFP60216
	c 37	16.4	1.7	23	ADG29459
	c 38	16.4	1.7	21	ADN34460
	c 39	16.4	1.7	21	ADH93721
	c 40	16.2	1.7	21	ADR32217
	c 41	16.2	1.7	21	ADM29439
	c 42	16.2	1.7	22	AAA91634
	c 43	16.2	1.7	22	AAH91288
	c 44	16.2	1.7	22	AA49459
	c 45	16.2	1.7	23	AAH56034
	c 46	16	1.6	20	ABZ92750
	c 47	16	1.6	20	Human forehead box
	c 48	15.8	1.6	19	ADP84188
	c 49	15.8	1.6	19	ADP83885
	c 50	15.8	1.6	20	AAQ85691
	c 51	15.8	1.6	20	AT89333
	c 52	15.8	1.6	20	ADN31411
	c 53	15.8	1.6	20	ADN31539
	c 54	15.8	1.6	21	ADK96735
	c 55	15.6	1.6	22	ADT33144
	c 56	15.6	1.6	22	ADQ76762
	c 57	15.4	1.6	17	ABN07601
	c 58	15.4	1.6	17	ACN70630
	c 59	15.4	1.6	17	ABV91103
	c 60	15.4	1.6	17	ABV91101
	c 61	15.4	1.6	17	ADT48552
	c 62	15.4	1.6	17	AC52241
	c 63	15.4	1.6	17	ACN70630
	c 64	15.4	1.6	20	AAC83280
	c 65	15.4	1.6	20	ADD56638
	c 66	15.4	1.6	20	ADH94177
	c 67	15.4	1.6	20	ADH50561
	c 68	15.4	1.6	20	ADN30050
	c 69	15.4	1.6	20	ADP71239
	c 70	15.4	1.6	22	ABX72480
	c 71	15.4	1.6	20	AA204738
	c 72	15.2	1.6	20	AAA11885
	c 73	15.2	1.6	20	AAAG6201
	c 74	15.2	1.6	20	ADK76030
	c 75	15.2	1.6	20	ADK75938
	c 76	15.2	1.6	20	ADJ10237
	c 77	15.2	1.6	20	ADU10345
	c 78	15.2	1.6	20	ADM14353
	c 79	15.2	1.6	20	ADN31530
	c 80	15.2	1.6	20	ADN31412
	c 81	15.2	1.6	20	ADP77448
	c 82	15.2	1.6	20	ADP77832
	c 83	15.2	1.6	20	ADP77258
	c 84	15.2	1.6	20	ADP77215
	c 85	15.2	1.6	20	ADQ09501
	c 86	15.2	1.6	20	ADQ09573
	c 87	15.2	1.6	20	ADP83566
	c 88	15.2	1.6	20	ADP68633
	c 89	15.2	1.6	20	ADK22538
	c 90	15.2	1.6	20	ADR72435
	c 91	15.2	1.6	21	AAQ84666
	c 92	15.2	1.6	21	AAAT34674
	c 93	15.2	1.6	21	AAX15019
	c 94	15.2	1.6	21	AAE64753
	c 95	15.2	1.6	21	AAL51986
	c 96	15.2	1.6	21	ACG06031
	c 97	15.2	1.6	21	ACG9378
	c 98	15.2	1.6	21	ACD13612
	c 99	15.2	1.6	21	AD030610
	c 100	15	1.5	17	ACB911022
	c 101	15	1.5	18	AAV33862
	c 102	15	1.5	18	AAK75966
	c 103	15	1.5	18	AD41987
	c 104	15	1.5	21	AAFP7228
	c 105	14.8	1.5	18	AAZ230583
	c 106	14.8	1.5	18	AAH62926

c 107	1.5	18	1	AAS10245	c 180	14.4	1.5	AAH95352
c 108	14.8	18	1	AAD20374	c 181	14.4	1.5	AAH95217
c 109	14.8	18	1	AAD41925	c 182	14.4	1.5	ABK03125
c 110	14.8	1.5	18	1	ABD51440	183	14.4	1.5
c 111	14.8	1.5	18	1	ADR44784	184	14.4	1.5
c 112	14.8	1.5	18	1	ADR44782	185	14.4	1.5
c 113	14.8	1.5	19	1	AAV08207	186	14.4	1.5
c 114	14.8	1.5	19	1	AD51141	187	14.4	1.5
c 115	14.8	1.5	19	1	ABX13143	188	14.4	1.5
c 116	14.8	1.5	19	1	AD018775	189	14.4	1.5
c 117	14.8	1.5	19	1	AD0133679	190	14.4	1.5
c 118	14.8	1.5	19	1	AD018575	191	14.4	1.5
c 119	14.8	1.5	19	1	AD01848	192	14.4	1.5
c 120	14.8	1.5	20	1	ADT01909	193	14.4	1.5
c 121	14.8	1.5	20	1	AAQ039534	194	14.4	1.5
c 122	14.8	1.5	20	1	AAQ82814	195	14.4	1.5
c 123	14.8	1.5	20	1	AT15114	196	14.4	1.5
c 124	14.8	1.5	20	1	AT15134	197	14.4	1.5
c 125	14.8	1.5	20	1	AV21006	198	14.4	1.5
c 126	14.8	1.5	20	1	AV21038	199	14.4	1.5
c 127	14.8	1.5	20	1	AV18196	c 200	14.4	1.5
c 128	14.8	1.5	20	1	AV21694	c 201	14.4	1.5
c 129	14.8	1.5	20	1	AAZ21662	c 202	14.4	1.5
c 130	14.8	1.5	20	1	AAZ01970	c 203	14.4	1.5
c 131	14.8	1.5	20	1	AAZ05591	c 204	14.4	1.5
c 132	14.8	1.5	20	1	AA09682	c 205	14.4	1.5
c 133	14.8	1.5	20	1	AACT73103	c 206	14.4	1.5
c 134	14.8	1.5	20	1	AAF85110	c 207	14.4	1.5
c 135	14.8	1.5	20	1	AA04029	c 208	14.4	1.5
c 136	14.8	1.5	20	1	AD22828	c 209	14.4	1.5
c 137	14.8	1.5	20	1	AB56890	c 210	14.4	1.5
c 138	14.8	1.5	20	1	ABX04357	c 211	14.4	1.5
c 139	14.8	1.5	20	1	ADC65775	c 212	14.4	1.5
c 140	14.8	1.5	20	1	ADC10441	c 213	14.4	1.5
c 141	14.8	1.5	20	1	AD62218	c 214	14.4	1.5
c 142	14.8	1.5	20	1	AB2993157	c 215	14.4	1.5
c 143	14.8	1.5	20	1	ABZ89595	c 216	14.4	1.5
c 144	14.8	1.5	20	1	ABZ91021	c 217	14.4	1.5
c 145	14.8	1.5	20	1	ACC83590	c 218	14.4	1.5
c 146	14.8	1.5	20	1	ABD32388	c 219	14.4	1.5
c 147	14.8	1.5	20	1	ABD22725	c 220	14.4	1.5
c 148	14.8	1.5	20	1	ADP22034	c 221	14.4	1.5
c 149	14.8	1.5	20	1	ADK95099	c 222	14.4	1.5
c 150	14.8	1.5	20	1	AD61242	c 223	14.4	1.5
c 151	14.8	1.5	20	1	AD046632	c 224	14.4	1.5
c 152	14.8	1.5	20	1	AD052426	c 225	14.4	1.5
c 153	14.8	1.5	20	1	AD052460	c 226	14.4	1.5
c 154	14.8	1.5	20	1	ADP22034	c 227	14.4	1.5
c 155	14.8	1.5	20	1	ADP21936	c 228	14.4	1.5
c 156	14.8	1.5	20	1	ADP83554	c 229	14.4	1.5
c 157	14.8	1.5	20	1	ADP83557	c 230	14.4	1.5
c 158	14.8	1.5	20	1	ABK95668	c 231	14.4	1.5
c 159	14.8	1.5	20	1	ABK95969	c 232	14.4	1.5
c 160	14.8	1.5	20	1	ABK95794	c 233	14.4	1.5
c 161	14.8	1.5	21	1	ABK95941	c 234	14.4	1.5
c 162	14.8	1.5	21	1	ABK95971	c 235	14.4	1.5
c 163	14.8	1.5	21	1	ABK95975	c 236	14.4	1.5
c 164	14.8	1.5	21	1	ABK95972	c 237	14.4	1.5
c 165	14.6	1.5	21	1	ABK95970	c 238	14.2	1.5
c 166	14.6	1.5	21	1	ABK95978	c 239	14.2	1.5
c 167	14.6	1.5	21	1	ABK95979	c 240	14.2	1.5
c 168	14.6	1.5	21	1	ABK95940	c 241	14.2	1.5
c 169	14.6	1.5	21	1	ABK95973	c 242	14.2	1.5
c 170	14.6	1.5	21	1	ABK95968	c 243	14.2	1.5
c 171	14.6	1.5	21	1	ABK95974	c 244	14.2	1.5
c 172	14.6	1.5	21	1	ABK95942	c 245	14.2	1.5
c 173	14.6	1.5	21	1	ABK95979	c 246	14.2	1.5
c 174	14.6	1.5	21	1	ABK95971	c 247	14.2	1.5
c 175	14.6	1.5	21	1	ABK95973	c 248	14.2	1.5
c 176	14.6	1.5	21	1	ABK95944	c 249	14.2	1.5
c 177	14.4	1.5	21	1	ABL42381	c 250	14.2	1.5
c 178	14.4	1.5	21	1	ABL44677	c 251	14.2	1.5
c 179	14.4	1.5	21	1	AAH95977	c 252	14.2	1.5

c 253	14.2	1.5	20	1	AAZ433821	Human fetal brain	Human PRO 300 PCR
c 254	14.2	1.5	20	1	AAZ229101	Forward primer new	Human PRO 300 PCR
c 255	14.2	1.5	20	1	AAZ885339	Human GFR-alpha-3	Human PRO 300 PCR
c 256	14.2	1.5	20	1	AAZ78613	Human PRO300 forward	Human PRO 300 PCR
c 257	14.2	1.5	20	1	AAZ77618	Human PRO338 PCR	Human PRO 300 PCR
c 258	14.2	1.5	20	1	AAZ49210	Human Tumour necro	Human PRO 300 PCR
c 259	14.2	1.5	20	1	AAZ54098	Primer for amplify	Human PRO 300 PCR
c 260	14.2	1.5	20	1	AAAC58151	Human PRO338 and P	Human PRO 300 PCR
c 261	14.2	1.5	20	1	AAZ87024	Sequencing primer	Human PRO 300 PCR
c 262	14.2	1.5	20	1	AAZ30531	PPAR-alpha Gene ex	Human PRO 300 PCR
c 263	14.2	1.5	20	1	AAH20646	Human telomeric re	Human PRO 300 PCR
c 264	14.2	1.5	20	1	AAH80522	Oligonucleotide hy	Human PRO 300 PCR
c 265	14.2	1.5	20	1	AAH80523	Oligonucleotide hy	Human PRO 300 PCR
c 266	14.2	1.5	20	1	ABA82191	Human Gene region	Human PRO 300 PCR
c 267	14.2	1.5	20	1	ADD36541	Human Her-1 antisie	Human PRO 300 PCR
c 268	14.2	1.5	20	1	AB52377	Mouse FLIP-c chime	Human PRO 300 PCR
c 269	14.2	1.5	20	1	AAZ38112	Human BCAS1 antisie	Human PRO 300 PCR
c 270	14.2	1.5	20	1	AAU49434	Cell adhesion mole	Human PRO 300 PCR
c 271	14.2	1.5	20	1	AAU49432	Cell adhesion mole	Human PRO 300 PCR
c 272	14.2	1.5	20	1	ABO81631	PGHS-2 sense prime	Human PRO 300 PCR
c 273	14.2	1.5	20	1	ABO81627	PGHS-1 sense prime	Human PRO 300 PCR
c 274	14.2	1.5	20	1	AB54275	Human chromosome 1	Human PRO 300 PCR
c 275	14.2	1.5	20	1	ABR43387	Sigle-BMS, PCR pr	Human PRO 300 PCR
c 276	14.2	1.5	20	1	ABT193019	Capture oligonucle	Human PRO 300 PCR
c 277	14.2	1.5	20	1	ACR63476	Novel human secret	Human PRO 300 PCR
c 278	14.2	1.5	20	1	ABT34154	Human short hetero	Human PRO 300 PCR
c 279	14.2	1.5	20	1	ACR71640	Human PRO Polypept	Human PRO 300 PCR
c 280	14.2	1.5	20	1	ABP92280	Human secreted/tra	Human PRO 300 PCR
c 281	14.2	1.5	20	1	ACR66021	HIV variant detect	Human PRO 300 PCR
c 282	14.2	1.5	20	1	ABT15981	Secreted and trans	Human PRO 300 PCR
c 283	14.2	1.5	20	1	ACD24560	Novel human secret	Human PRO 300 PCR
c 284	14.2	1.5	20	1	ACD29622	Novel secreted/cra	Human PRO 300 PCR
c 285	14.2	1.5	20	1	ACD12221	Novel 1 human secret	Human PRO 300 PCR
c 286	14.2	1.5	20	1	ACD29037	Clone specific PCR	Human PRO 300 PCR
c 287	14.2	1.5	20	1	ACD65822	HIV variant detect	Human PRO 300 PCR
c 288	14.2	1.5	20	1	ACD73527	Novel human secret	Human PRO 300 PCR
c 289	14.2	1.5	20	1	ACD76243	Novel human secret	Human PRO 300 PCR
c 290	14.2	1.5	20	1	ACD43669	Novel human secret	Human PRO 300 PCR
c 291	14.2	1.5	20	1	ACD61429	Novel human secret	Human PRO 300 PCR
c 292	14.2	1.5	20	1	ACD63393	Human PRO 300 PCR	Human PRO 300 PCR
c 293	14.2	1.5	20	1	ACD66493	Human PRO 300 PCR	Human PRO 300 PCR
c 294	14.2	1.5	20	1	ACD68617	Human PRO 300 PCR	Human PRO 300 PCR
c 295	14.2	1.5	20	1	ACD62677	Human PRO 300 PCR	Human PRO 300 PCR
c 296	14.2	1.5	20	1	ACD67742	HIV PRT antisense	Human PRO 300 PCR
c 297	14.2	1.5	20	1	ACD41062	HIV PRT antisense	Human PRO 300 PCR
c 298	14.2	1.5	20	1	ACD67117	Human PRO 300 PCR	Human PRO 300 PCR
c 299	14.2	1.5	20	1	ACD62053	Human PRO 300 PCR	Human PRO 300 PCR
c 300	14.2	1.5	20	1	ACD41686	Human PRO 300 PCR	Human PRO 300 PCR
c 301	14.2	1.5	20	1	ACD849055	HIV PRT antisense	Human PRO 300 PCR
c 302	14.2	1.5	20	1	ACD81414	PCR primer (SEQ ID	Human PRO 300 PCR
c 303	14.2	1.5	20	1	AD081413	PCR primer (SEQ ID	Human PRO 300 PCR
c 304	14.2	1.5	20	1	AD335109	Human oligonucleot	Human PRO 300 PCR
c 305	14.2	1.5	20	1	ADE16223	Human oligonucleot	Human PRO 300 PCR
c 306	14.2	1.5	20	1	ADD72838	Novel human secret	Human PRO 300 PCR
c 307	14.2	1.5	20	1	ADD72196	Intestinal epithel	Human PRO 300 PCR
c 308	14.2	1.5	20	1	AD1606938	AA626628-derived O	Human PRO 300 PCR
c 309	14.2	1.5	20	1	ABZ21282	AA626628-derived O	Human PRO 300 PCR
c 310	14.2	1.5	20	1	ABZ93292	AA626628-derived O	Human PRO 300 PCR
c 311	14.2	1.5	20	1	ADP46861	AA626628-derived O	Human PRO 300 PCR
c 312	14.2	1.5	20	1	ADG52618	AA626628-derived O	Human PRO 300 PCR
c 313	14.2	1.5	20	1	ACD42441	AA626628-derived O	Human PRO 300 PCR
c 314	14.2	1.5	20	1	AD124968	AA626628-derived O	Human PRO 300 PCR
c 315	14.2	1.5	20	1	ABD29731	AA626628-derived O	Human PRO 300 PCR
c 316	14.2	1.5	20	1	ABD29522	AA626628-derived O	Human PRO 300 PCR
c 317	14.2	1.5	20	1	ABZ93501	AA626628-derived O	Human PRO 300 PCR
c 318	14.2	1.5	20	1	ADT00450	Novel mutant prote	Human PRO 300 PCR
c 319	14.2	1.5	20	1	ADT00459	Novel mutant prote	Human PRO 300 PCR
c 320	14.2	1.5	20	1	ADT94303	Novel mutant prote	Human PRO 300 PCR
c 321	14.2	1.5	20	1	ADP44875	Novel mutant prote	Human PRO 300 PCR
c 322	14.2	1.5	20	1	ADT00459	Novel mutant prote	Human PRO 300 PCR
c 323	14.2	1.5	20	1	ABN07587	Novel mutant prote	Human PRO 300 PCR
c 324	14.2	1.5	20	1	ABN07588	Novel mutant prote	Human PRO 300 PCR
c 325	14.2	1.5	20	1	ABN07711	Novel mutant prote	Human PRO 300 PCR
c 326	14.2	1.5	20	1	ADF61096	Human GFR-alpha-3	Human PRO 300 PCR
c 327	14.2	1.5	20	1	ADF39788	Human GFR-alpha-3	Human PRO 300 PCR
c 328	14.2	1.5	20	1	ADP45584	Human GFR-alpha-3	Human PRO 300 PCR
c 329	14.2	1.5	20	1	ADF23980	Human GFR-alpha-3	Human PRO 300 PCR
c 330	14.2	1.5	20	1	ADF40412	Human GFR-alpha-3	Human PRO 300 PCR
c 331	14.2	1.5	20	1	ADF23356	Human GFR-alpha-3	Human PRO 300 PCR
c 332	14.2	1.5	20	1	ADF23339	Human GFR-alpha-3	Human PRO 300 PCR
c 333	14.2	1.5	20	1	ADF26806	Human GFR-alpha-3	Human PRO 300 PCR
c 334	14.2	1.5	20	1	ADF27142	Human GFR-alpha-3	Human PRO 300 PCR
c 335	14.2	1.5	20	1	ADF41036	Human GFR-alpha-3	Human PRO 300 PCR
c 336	14.2	1.5	20	1	ADG33755	Human GFR-alpha-3	Human PRO 300 PCR
c 337	14.2	1.5	20	1	ADG25081	Human GFR-alpha-3	Human PRO 300 PCR
c 338	14.2	1.5	20	1	ADG26112	Human GFR-alpha-3	Human PRO 300 PCR
c 339	14.2	1.5	20	1	ADF33391	Human GFR-alpha-3	Human PRO 300 PCR
c 340	14.2	1.5	20	1	ADG46208	MSH6 gene specific	Human PRO 300 PCR
c 341	14.2	1.5	20	1	ADG50818	Human GFR-alpha-3	Human PRO 300 PCR
c 342	14.2	1.5	20	1	ADG58762	Human GFR-alpha-3	Human PRO 300 PCR
c 343	14.2	1.5	20	1	ADG52218	Human GFR-alpha-3	Human PRO 300 PCR
c 344	14.2	1.5	20	1	ADG48946	Human GFR-alpha-3	Human PRO 300 PCR
c 350	14.2	1.5	20	1	ADG48322	Human GFR-alpha-3	Human PRO 300 PCR
c 351	14.2	1.5	20	1	ADH65573	Human GFR-alpha-3	Human PRO 300 PCR
c 352	14.2	1.5	20	1	ADH63740	Human GFR-alpha-3	Human PRO 300 PCR
c 353	14.2	1.5	20	1	ADJ78377	Human GFR-alpha-3	Human PRO 300 PCR
c 360	14.2	1.5	20	1	ADJ18023	Antisense DNA olig	Human PRO 300 PCR
c 361	14.2	1.5	20	1	ADJ18234	Antisense DNA olig	Human PRO 300 PCR
c 362	14.2	1.5	20	1	ADJ18519	Antisense DNA olig	Human PRO 300 PCR
c 363	14.2	1.5	20	1	ADJ78447	Chimeric phosphoro	Human PRO 300 PCR
c 364	14.2	1.5	20	1	ADK75814	Chimeric phosphoro	Human PRO 300 PCR
c 365	14.2	1.5	20	1	ADK76483	Chimeric phosphoro	Human PRO 300 PCR
c 366	14.2	1.5	20	1	ADK75583	Chimeric phosphoro	Human PRO 300 PCR
c 367	14.2	1.5	20	1	ADK75554	Chimeric phosphoro	Human PRO 300 PCR
c 368	14.2	1.5	20	1	ADM17020	Human PIM-1 DNA an	Human PRO 300 PCR
c 370	14.2	1.5	20	1	ADL06834	Human PIM-1 DNA an	Human PRO 300 PCR
c 371	14.2	1.5	20	1	ADM14424	Human PIM-1 DNA an	Human PRO 300 PCR
c 372	14.2	1.5	20	1	ADK76483	4 synthesis-period	Human PRO 300 PCR
c 373	14.2	1.5	20	1	ADP54014	Farnesoid X recept	Human PRO 300 PCR
c 374	14.2	1.5	20	1	ADN03050	Farnesoid X recept	Human PRO 300 PCR
c 375	14.2	1.5	20	1	ADN03079	Human PIM-1 DNA an	Human PRO 300 PCR
c 376	14.2	1.5	20	1	ADN03148	Human PIM-1 DNA an	Human PRO 300 PCR
c 377	14.2	1.5	20	1	ADP78345	Human NRF antisens	Human PRO 300 PCR
c 378	14.2	1.5	20	1	ADP78490	Human NRF antisens	Human PRO 300 PCR
c 379	14.2	1.5	20	1	ADK20894	Human PIM-1 DNA an	Human PRO 300 PCR
c 380	14.2	1.5	20	1	ADK22640	Chimeric phosphoro	Human PRO 300 PCR
c 381	14.2	1.5	20	1	ADP27889	Chimeric phosphoro	Human PRO 300 PCR
c 382	14.2	1.5	20	1	ADK21310	Acyl-coenzyme A sy	Human PRO 300 PCR
c 383	14.2	1.5	20	1	ADP74572	Acyl-coenzyme A sy	Human PRO 300 PCR
c 384	14.2	1.5	20	1	ADP86633	Acyl-coenzyme A sy	Human PRO 300 PCR
c 385	14.2	1.5	20	1	ADR00341	Acyl-coenzyme A sy	Human PRO 300 PCR
c 386	14.2	1.5	20	1	ADT00450	Novel mutant prote	Human PRO 300 PCR
c 387	14.2	1.5	20	1	ADT00459	Novel mutant prote	Human PRO 300 PCR
c 388	14.2	1.5	20	1	ADT94303	Novel mutant prote	Human PRO 300 PCR
c 389	14.2	1.5	20	1	ADR44875	Novel mutant prote	Human PRO 300 PCR
c 390	14.2	1.5	20	1	AAV18737	Primer for HRSV	Human PRO 300 PCR
c 391	14.2	1.5	20	1	ABN07587	Human GDMLe-1 17-m	Human PRO 300 PCR
c 392	14.2	1.5	20	1	ABN07587	Human GDMLe-1 17-m	Human PRO 300 PCR
c 393	14.2	1.5	20	1	ABD29731	Human GDMLe-1 17-m	Human PRO 300 PCR
c 394	14.2	1.5	20	1	ABD29522	Human GDMLe-1 17-m	Human PRO 300 PCR
c 395	14.2	1.5	20	1	ABD29522	Human GDMLe-1 17-m	Human PRO 300 PCR
c 396	14.2	1.5	20	1	ABD29522	Human GDMLe-1 17-m	Human PRO 300 PCR
c 397	14.2	1.5	20	1	ABD29522	Human GDMLe-1 17-m	Human PRO 300 PCR
c 398	14.2	1.5	20	1	ABD29522	Human GDMLe-1 17-m	Human PRO 300 PCR

c 399	1.4	17	1	ABN07712	Human GDMLP-1 17-m	c 472	13.8	1.4	18	1	AAT51719
c 400	1.4	17	1	ACN66338	Murine Oligonucleo	473	13.8	1.4	18	1	AAH47533
c 401	1.4	17	1	ACN70802	Human GDMLP-1 prob	474	13.8	1.4	18	1	ACF62165
c 402	1.4	17	1	ACN70801	Human GDMLP-1 prob	475	13.8	1.4	18	1	ACF62766
c 403	1.4	17	1	ACN70888	Human GDMLP-1 prob	476	13.8	1.4	18	1	ADM06739
c 404	1.4	17	1	ACN70887	Human GDMLP-1 prob	477	13.8	1.4	18	1	ABD20008
c 405	1.4	18	1	AT50908	Probe SH-10 for HS	478	13.8	1.4	18	1	ADH32525
c 406	1.4	18	1	AT70004	Probe SH-10 for HS	479	13.8	1.4	19	1	AAT76395
c 407	1.4	18	1	ATX54336	C/EBP-beta antisense	480	13.8	1.4	19	1	PAR0820
c 408	1.4	18	1	AAA34283	Human adenosine re	481	13.8	1.4	19	1	AAV08220
c 409	1.4	18	1	ADR20405	Human C/EBP polyunu	482	13.8	1.4	19	1	AAV72612
c 410	1.4	18	1	ABZ96039	Human C/EBP antisense	483	13.8	1.4	19	1	AAK65350
c 411	1.4	19	1	ATX54335	C/EBP-beta antisense	484	13.8	1.4	19	1	AAK54544
c 412	1.4	19	1	AAA34282	Human adenosine re	485	13.8	1.4	19	1	AAA33988
c 413	1.4	19	1	AP20404	Human C/EBP polyunu	486	13.8	1.4	19	1	AAK83068
c 414	1.4	19	1	ABZ96038	Human C/EBP antisense	487	13.8	1.4	19	1	AAA33572
c 415	1.4	19	1	ATX54348	Human apolipoprote	488	13.8	1.4	19	1	AAA86016
c 416	1.4	19	1	ADR75588	Human apolipoprote	489	13.8	1.4	19	1	AAK84481
c 417	1.4	19	1	ADR78246	Human apolipoprote	490	13.8	1.4	19	1	AAF20110
c 418	1.4	19	1	AAA34284	Human apolipoprote	491	13.8	1.4	19	1	AAH58230
c 419	1.4	19	1	ATX54334	C/EBP-beta antisense	492	13.8	1.4	19	1	AAH88734
c 420	1.4	19	1	ATX92168	PCR Primer used to	493	13.8	1.4	19	1	AAH61178
c 421	1.4	20	1	AAA34281	Human adenosine re	494	13.8	1.4	19	1	AAH59643
c 422	1.4	20	1	ABD20409	Murine TNFalpha antisense	495	13.8	1.4	19	1	ADA25500
c 423	1.4	20	1	AAA40869	Human C/EBP polyunu	496	13.8	1.4	19	1	ADA5375
c 424	1.4	20	1	AAF20403	Tumour necrosis fa	497	13.8	1.4	19	1	ADE23876
c 425	1.4	20	1	ATD05697	Primer for amplify	498	13.8	1.4	19	1	ADE29771
c 426	1.4	20	1	ATD42478	Human oligonucleot	499	13.8	1.4	19	1	ADE30106
c 427	1.4	20	1	ABZ96037	Human C/EBP antisense	500	13.8	1.4	19	1	ADE30097
c 428	1.4	20	1	ABD21439	Human transglutami	501	13.8	1.4	19	1	ADE39624
c 429	1.4	20	1	ADP27218	Human MMPI DNA antisense	502	13.8	1.4	19	1	ADP7519
c 430	1.4	20	1	ADP27133	Human matrix metal	503	13.8	1.4	19	1	ADP75534
c 431	1.4	20	1	ADP29179	Mouse TNF alpha antisense	504	13.8	1.4	19	1	ADG35531
c 432	1.4	20	1	ADP28520	Human oligonucleot	505	13.8	1.4	19	1	ADG5292
c 433	1.4	20	1	ABZ96039	Delta-9 desaturase	506	13.8	1.4	19	1	ADG16269
c 434	1.4	20	1	ATX62853	Human genomic SNP	507	13.8	1.4	19	1	ADG36030
c 435	1.4	20	1	ABD20401	Human CD20 Amberzy	508	13.8	1.4	19	1	ABZ95804
c 436	1.4	20	1	ATD03651	Human GRID NCH	509	13.8	1.4	19	1	ABD20007
c 437	1.4	20	1	ATD03692	Human GRID NCH	510	13.8	1.4	19	1	ABD19544
c 438	1.4	20	1	ATD02695	Human GRID Amberzy	511	13.8	1.4	19	1	ADQ22943
c 439	1.4	20	1	ATX62853	Human GDMLP-1 17-m	512	13.8	1.4	19	1	ADQ24077
c 440	1.4	20	1	ABN07596	Human GDMLP-1 17-m	513	13.8	1.4	19	1	ABK52977
c 441	1.4	20	1	ABN01495	Human GDMLP-1 17-m	514	13.8	1.4	16	1	AK51838
c 442	1.4	20	1	ABN07595	Human GDMLP-1 17-m	515	13.8	1.4	16	1	AA43285
c 443	1.4	20	1	ABN07715	Human GDMLP-1 17-m	516	13.8	1.4	16	1	AAE40407
c 444	1.4	20	1	ABL47134	Human KITM1 port1	517	13.8	1.4	16	1	ABZ26101
c 445	1.4	20	1	ATB36354	Tumour suppression	518	13.8	1.4	17	1	AAK54837
c 446	1.4	20	1	ATC09002	NFKB sub-unit modu	519	13.8	1.4	20	1	AAK44284
c 447	1.4	20	1	ACA09005	NFKB sub-unit modu	520	13.8	1.4	17	1	AAF20406
c 448	1.4	20	1	ACG64648	NFKB sub-unit modu	521	13.8	1.4	17	1	ABZ96100
c 449	1.4	20	1	ABD00532	Human MN23 scaninin	522	13.8	1.4	20	1	ABD29357
c 450	1.4	20	1	ABD00533	Murine oligonucleo	523	13.8	1.4	20	1	ABD32388
c 451	1.4	20	1	ABD0054	Murine oligonucleo	524	13.8	1.4	20	1	ADJ61242
c 452	1.4	20	1	ATC65263	Tumour suppression	525	13.8	1.4	20	1	AAK74793
c 453	1.4	20	1	ATC64648	Murine oligonucleo	526	13.8	1.4	17	1	ABK03469
c 454	1.4	20	1	ATC63330	Murine oligonucleo	527	13.8	1.4	17	1	AAK75320
c 455	1.4	20	1	ATC63843	Murine oligonucleo	528	13.8	1.4	16	1	AAK74956
c 456	1.4	20	1	ATC63438	Rat P11 mutagenic	529	13.4	1.4	16	1	AAV97492
c 457	1.4	20	1	ATC63167	Human GRID mRNA	530	13.4	1.4	17	1	AAK57838
c 458	1.4	20	1	ATC63585	Human GDMLP-1 prob	531	13.4	1.4	17	1	AAH95216
c 459	1.4	20	1	ATC70806	Human GDMLP-1 prob	532	13.4	1.4	17	1	AAK74957
c 460	1.4	20	1	ATD149425	Human GDMLP-1 prob	533	13.4	1.4	17	1	AAH91135
c 461	1.4	20	1	ATD149372	Human tumour suppr	534	13.4	1.4	17	1	ABN07603
c 462	1.4	20	1	ATB13141	Rat P11 mutagenic	535	13.4	1.4	17	1	ABN0494
c 463	1.4	20	1	ATD4040	Human GRID mRNA	536	13.4	1.4	17	1	ABN0493
c 464	1.4	20	1	ATB41320	Tumour suppression	537	13.4	1.4	17	1	ABQ53741
c 465	1.4	20	1	ATD150598	Human GDMLP-1 prob	538	13.4	1.4	17	1	ABQ63740
c 466	1.4	20	1	ATC63630	Human GDMLP-1 prob	539	13.4	1.4	17	1	ABQ63740
c 467	1.4	20	1	ATC63739	Human GDMLP-1 prob	540	13.4	1.4	17	1	ABQ63740
c 468	1.4	20	1	ATC63585	Human GDMLP-1 prob	541	13.4	1.4	17	1	ABQ63740
c 469	1.4	20	1	ATD74696	Common Primer for	542	13.4	1.4	17	1	ABQ63741
c 470	1.4	20	1	ATC39740	rev-AS (2328) anti	543	13.4	1.4	17	1	ABQ63740
c 471	1.4	20	1	ATAT43031	Juvenile glaucoma	544	13.4	1.4	17	1	ABQ63740

c 545	1.4	17	1	ABV91099	Human POSH1L1 scann	1	ADD26423
c 546	1.4	17	1	ABV91105	Human POSH1L1 scann	1	ACF58897
c 547	1.4	17	1	ABT37970	Tumour suppression	1	ADH69529
c 548	1.4	17	1	ABT38045	Tumour suppression	1	ABT23665
c 549	1.4	17	1	ABT39267	Tumour suppression	1	ABT23556
c 550	1.4	17	1	ABZ61864	Human H-Ras DNazym	1	AD15848
c 551	1.4	17	1	ABZ61330	Human H-Ras DNazym	1	ADM69761
c 552	1.4	17	1	ACG66009	Murine oligonucleo	1	ADR47462
c 553	1.4	17	1	ACG64573	Murine oligonucleo	1	ADR48113
c 554	1.4	17	1	ACG64668	Murine oligonucleo	1	ABN26626
c 555	1.4	17	1	ACG68975	LRP5 mutagenic PCR	1	ABF28359
c 562	1.4	17	1	ABD20009	Tumour suppression	1	ABF28558
c 563	1.4	17	1	ABD41073	Human C/EBP β DNA f	1	ABK95764
c 557	1.4	17	1	ABD43229	Human GDMLP-1 ProB	1	AAH94577
c 558	1.4	17	1	ABD40679	Tumour suppression	1	ABK95976
c 559	1.4	17	1	ABD44571	Tumour suppression	1	ABK9543
c 560	1.4	17	1	ADT51271	Human tumour suppr	1	ADS91058
c 561	1.4	17	1	ACG52645	Human tumour suppr	1	AAT81210
c 562	1.4	17	1	ACG52645	Human C/EBP β DNA f	1	AAT60343
c 563	1.4	17	1	ACN70693	Human GDMLP-1 ProB	1	AA36322
c 564	1.4	17	1	ACN63584	Human GDMLP-1 ProB	1	AAH94577
c 565	1.4	17	1	ACN63583	Human GDMLP-1 ProB	1	ABH94577
c 566	1.4	17	1	ADT50609	Human CETP hairpin	1	ABN07710
c 567	1.4	18	1	AAU50708	Rabbit CETP hairpi	1	ACN07867
c 568	1.4	18	1	AAU73000	Human biallelic ma	1	ACN12552
c 569	1.4	18	1	AAZ75130	Human biallelic ma	1	ACN10138
c 570	1.4	18	1	AAU52046	Antisense Oligonuc	1	ACN03003
c 571	1.4	18	1	AAU41001	Human PI3K p85 ant	1	ACN05107
c 572	1.4	18	1	ABT12998	Human cytochrome C	1	ACN03020
c 573	1.4	18	1	AAU55147	PGC-1 mutational a	1	ACN14428
c 574	1.4	18	1	ADN06576	Human PCR primer S	1	ABT39774
c 575	1.4	18	1	ADN06437	Human PCR primer S	1	ABT38307
c 576	1.4	18	1	ADU38158	Plastid division-r	1	ACA05633
c 577	1.4	18	1	AAU82434	cdk1 ribozyme bind	1	ACA06537
c 578	1.4	19	1	AAU87029	Sequencing primer	1	ADB42338
c 579	1.4	19	1	AAU15514	SNP specific upper	1	ADB45862
c 580	1.4	19	1	AAUH37681	Cell-cycle depende	1	ADB48000
c 581	1.4	19	1	AAUH7596	A. thaliana metal	1	AD148149
c 582	1.4	19	1	AAUH76184	Sense PCR primer u	1	ACBQ84437
c 583	1.4	19	1	AAUH6601	Human VEGFR3 short	1	Human NOVX protein
c 584	1.4	19	1	AAUH37698	Human VEGFR3 short	1	Human glioma endot
c 585	1.4	19	1	AAUH16597	Human BACE siNA 10	1	ADK13120
c 586	1.4	19	1	ADH16272	Human BACE transcr	1	AD04210
c 587	1.4	19	1	ABY776184	TGF β 1 promoter T-	1	ADT70003
c 588	1.4	19	1	ADU6601	Human PDGF τ -target	1	ACN70800
c 589	1.4	19	1	ADP37451	Human PDGF τ -target	1	ABL31588
c 590	1.4	19	1	ADU015167	Protein tyrosine P	1	ACC83808
c 591	1.4	19	1	ADQ27663	RNA interference t	1	ADP46319
c 592	1.4	18	1	AAQ01367	Monomer DRB1002 fo	1	AAQ59546
c 593	1.4	18	1	AAQ55068	Sequence of fragme	1	ADR43841
c 594	1.4	18	1	AAU56750	Mouse TNF- α ha	1	ADT70003
c 595	1.4	18	1	AAU02860	Human EGR-1 DNA an	1	AAV75131
c 596	1.4	18	1	AAV14198	Human biallelic ma	1	Mouse flt-1/VEGF r
c 597	1.4	18	1	AAU03785	Human C5 gene anti	1	Delta-9 desaturase
c 598	1.4	18	1	AAU20992	TRADD gene antisense	1	Human IL-2 receptor
c 599	1.4	18	1	AAU944132	Human Rhoc phospho	1	Beta-galactosidase
c 600	1.4	18	1	AAU272009	Human EGFR-1 DNA an	1	Human thioredoxin
c 601	1.4	18	1	AAU52269	Human C5 antisense	1	Human estrogen receptor
c 602	1.4	18	1	AAU99734	Human Zmax1 cDNA r	1	Human Fc γ receptor
c 603	1.4	18	1	AAU293479	Human Akt-3 antisense	1	Human CFTR mutation corr
c 604	1.4	18	1	AAU79609	Human Rhoc phospho	1	Hammerhead ribozym
c 605	1.4	18	1	AAU94713	Human EGFR-1 DNA an	1	Hammerhead ribozym
c 606	1.4	18	1	AAU09729	Human C5 gene antisense	1	Hammerhead ribozym
c 607	1.4	18	1	ABA2519	Human Zmax1 gene region	1	Hammerhead ribozym
c 608	1.4	18	1	ABA23316	Human C5 gene antisense	1	Hammerhead ribozym
c 609	1.4	18	1	ABA05049	Human IgM heavy ch	1	Hammerhead ribozym
c 610	1.4	18	1	ABA06048	Human IgM heavy ch	1	Hammerhead ribozym
c 611	1.4	18	1	ABA130592	Human HLA genotypi	1	Hammerhead ribozym
c 612	1.4	18	1	ABA1287	Human C6ST gene am	1	Hammerhead ribozym
c 613	1.4	18	1	ABA274876	Human carnitine tr	1	Hammerhead ribozym
c 614	1.4	18	1	ACG45899	Human HBM STS mark	1	Primer used to amp
c 615	1.4	18	1	ACD19636	Human obesity rela	1	Long human Tumour
c 616	1.4	18	1	ACB92158	Sequence tagged si	1	Long human Tumour
c 617	1.4	18	1	ACD02807	Ex vivo stem-cell	1	Human GRID DNAyme

691	1.3	17	1	ABN07594	764	12.8	1.3	17	1	ABX72083	
692	12.8	1.3	17	1	ABQ6196	765	12.8	1.3	17	1	ABX72082
693	12.8	1.3	17	1	ABQ61738	766	12.8	1.3	17	1	ADL7061
c 694	12.8	1.3	17	1	ADD24250	767	12.8	1.3	17	1	ADL48439
c 695	12.8	1.3	17	1	ABK19447	768	12.8	1.3	17	1	ADL46632
c 696	12.8	1.3	17	1	ABK18886	769	12.8	1.3	17	1	ADL48316
c 697	12.8	1.3	17	1	ABK17494	770	12.8	1.3	17	1	ADL48867
c 698	12.8	1.3	17	1	ABK17493	771	12.8	1.3	17	1	ADMS45221
c 699	12.8	1.3	17	1	ABL31707	772	12.8	1.3	17	1	ADMS396
c 700	12.8	1.3	17	1	ABK56151	773	12.8	1.3	17	1	ADM54181
c 701	12.8	1.3	17	1	ABK53380	774	12.8	1.3	17	1	ADK13141
c 702	12.8	1.3	17	1	ABK56152	775	12.8	1.3	17	1	ACN70684
c 703	12.8	1.3	17	1	ACN06328	c 776	12.8	1.3	17	1	AD185172
c 704	12.8	1.3	17	1	ACN14786	c 777	12.8	1.3	17	1	AD165171
c 705	12.8	1.3	17	1	ACN0329	c 778	12.8	1.3	17	1	AD186672
c 706	12.8	1.3	17	1	ACN08557	c 779	12.8	1.3	17	1	ADL60409
c 707	12.8	1.3	17	1	ACN2684	c 780	12.8	1.3	17	1	ACNE3586
c 708	12.8	1.3	17	1	ACN02796	c 781	12.8	1.3	17	1	AAV63398
c 709	12.8	1.3	17	1	ACN02364	c 782	12.8	1.3	17	1	ACN70807
c 710	12.8	1.3	17	1	ACN00700	c 783	12.8	1.3	18	1	AAQ70337
c 711	12.8	1.3	17	1	ACN10982	c 784	12.8	1.3	18	1	AAQ82167
c 712	12.8	1.3	17	1	ABT36748	c 785	12.8	1.3	18	1	AAI28317
c 713	12.8	1.3	17	1	ABT35570	c 786	12.8	1.3	18	1	AAV08122
c 714	12.8	1.3	17	1	ACA07755	c 787	12.8	1.3	18	1	PRimer Vbta10 for
c 715	12.8	1.3	17	1	ACA06470	c 788	12.8	1.3	18	1	H. contortus PGP-O
c 716	12.8	1.3	17	1	ACA06471	c 789	12.8	1.3	18	1	Immuno-suppressant
c 717	12.8	1.3	17	1	ACA06516	c 790	12.8	1.3	18	1	Shed2 antisense 01
c 718	12.8	1.3	17	1	ACA06464	c 791	12.8	1.3	18	1	Human biallalic ma
c 719	12.8	1.3	17	1	ACA07747	c 792	12.8	1.3	18	1	Human leukocyte an
c 720	12.8	1.3	17	1	ABD05329	c 793	12.8	1.3	18	1	TRADD antisense 01
c 721	12.8	1.3	17	1	ABD05330	c 794	12.8	1.3	18	1	SPACERW Oligonucle
c 722	12.8	1.3	17	1	ABD00051	c 795	12.8	1.3	18	1	Spacer used in CRC
c 723	12.8	1.3	17	1	ABD00055	c 796	12.8	1.3	18	1	Human Her-3 mRNA 1
c 724	12.8	1.3	17	1	ABD05156	c 797	12.8	1.3	18	1	Primer used to seq
c 725	12.8	1.3	17	1	ABD0515	c 798	12.8	1.3	18	1	Drosophila ubx Gen
c 726	12.8	1.3	17	1	ABD61238	c 799	12.8	1.3	18	1	Trailin PCR primer
c 727	12.8	1.3	17	1	ABZ59953	c 800	12.8	1.3	18	1	Immunostimulatory
c 728	12.8	1.3	17	1	ABZ59954	c 801	12.8	1.3	18	1	AAF59483
c 729	12.8	1.3	17	1	ABZ6094	c 802	12.8	1.3	18	1	ABV72663
c 730	12.8	1.3	17	1	ABZ65504	c 803	12.8	1.3	18	1	ABST8144
c 731	12.8	1.3	17	1	ABZ61554	c 804	12.8	1.3	18	1	AAP81096
c 732	12.8	1.3	17	1	ABZ62204	c 805	12.8	1.3	18	1	AAL19065
c 733	12.8	1.3	17	1	ABZ64571	c 806	12.8	1.3	18	1	ABU53380
c 734	12.8	1.3	17	1	ABD61605	c 807	12.8	1.3	18	1	AAI70552
c 735	12.8	1.3	17	1	ACD61063	c 808	12.8	1.3	18	1	Human multidrug re
c 736	12.8	1.3	17	1	ACD61064	c 809	12.8	1.3	18	1	Mouse Lpin2 gene 3
c 737	12.8	1.3	17	1	ACD61618	c 810	12.8	1.3	18	1	Haematopoietic cel
c 738	12.8	1.3	17	1	ACD61606	c 811	12.8	1.3	18	1	Immunostimulatory
c 739	12.8	1.3	17	1	ACCD65305	c 812	12.8	1.3	18	1	DNA encoding human
c 740	12.8	1.3	17	1	ACCD61234	c 813	12.8	1.3	18	1	Immunostimulatory
c 741	12.8	1.3	17	1	ACCD67719	c 814	12.8	1.3	18	1	ADDB36975
c 742	12.8	1.3	17	1	ACCD65436	c 815	12.8	1.3	18	1	ADG27380
c 743	12.8	1.3	17	1	ACD6442	c 816	12.8	1.3	18	1	ADDB3217
c 744	12.8	1.3	17	1	ACCD63424	c 817	12.8	1.3	18	1	ADDB34055
c 745	12.8	1.3	17	1	ACCD65199	c 818	12.8	1.3	18	1	ADBF17412
c 746	12.8	1.3	17	1	ACD642193	c 819	12.8	1.3	18	1	ADQ99389
c 747	12.8	1.3	17	1	ACD642709	c 820	12.8	1.3	18	1	ADQ993570
c 748	12.8	1.3	17	1	ACD64415	c 821	12.8	1.3	18	1	ADK15543
c 749	12.8	1.3	17	1	ACD03734	c 822	12.8	1.3	18	1	ADW76163
c 750	12.8	1.3	17	1	ACD61390	c 823	12.8	1.3	18	1	AAX54839
c 751	12.8	1.3	17	1	ADG70291	c 824	12.8	1.3	18	1	ADW76994
c 752	12.8	1.3	17	1	ADB44781	c 825	12.8	1.3	18	1	ADK17529
c 753	12.8	1.3	17	1	ADB44421	c 826	12.8	1.3	18	1	ADT32230
c 754	12.8	1.3	17	1	ACD98198	c 827	12.6	1.3	13	1	ABH33279
c 755	12.8	1.3	17	1	ADF61389	c 828	12.6	1.3	13	1	ABH34778
c 756	12.8	1.3	17	1	ACD61399	c 829	12.6	1.3	13	1	ACD93373
c 757	12.8	1.3	17	1	ADG70291	c 830	12.6	1.3	15	1	AAI34286
c 758	12.8	1.3	17	1	AD152105	c 831	12.6	1.3	15	1	AAFP0408
c 759	12.8	1.3	17	1	AD15039	c 832	12.6	1.3	15	1	ABK81347
c 760	12.8	1.3	17	1	ADI48914	c 833	12.6	1.3	15	1	ABZ56102
c 761	12.8	1.3	17	1	ACCS5597	c 834	12.6	1.3	17	1	ABZ56684
c 762	12.8	1.3	17	1	ACCS5030	c 835	12.6	1.3	19	1	ABY13143
c 763	12.8	1.3	17	1	ACCS5357	c 836	12.6	1.3	20	1	ADDS24266

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OM nucleic - nucleic search, using sw model

Run on: June 27, 2005, 16:55:02 ; Search time 8 Seconds

(without alignments)

3.429 Million cell updates/sec

Title: us-09-915-814-3

Perfect score: 970

Sequence: 1 ctctgttaaaggaggtgta.....tttctgagtgggtcgccat 970

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 805 seqs, 14141 residues

Total number of hits satisfying chosen parameters:

1610

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 807 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Accession: E13893

Accession: CQ627745

Accession: CQ627746

Accession: AR468808

Accession: AR468809

Accession: AR468810

Accession: I152277

Accession: AR295250

Accession: AX031665

Accession: AR231756

Accession: AX181869

Accession: AX591252

Accession: AX164418

Accession: A81881

Accession: AR120684

Accession: BD135550

Accession: AR266660

Accession: CQ622852

Accession: CQ622853

Accession: AR469115

Accession: AR469116

Accession: AX532305

Accession: AX532307

Accession: AX672563

Accession: AX73475

Accession: B15095

Accession: AX962802

Accession: AX36176

Accession: BD23194

Accession: BD232554

Accession: AR361588

Accession: AX009496

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C	36	15.2	1.6	21	1	E11006
C	37	15.2	1.6	21	1	I34868
C	38	15.2	1.6	21	1	I88642
C	39	15.2	1.6	21	1	AR264510
C	40	15	1.5	17	1	AX532306
C	41	15	1.5	18	1	BD191371
C	42	15	1.5	18	1	AR260472
C	43	15	1.5	18	1	BD085312
C	44	14.8	1.5	18	1	AR080724
C	45	14.8	1.5	18	1	AR162707
C	46	14.8	1.5	18	1	BD227767
C	47	14.8	1.5	19	1	AX659161
C	48	14.8	1.5	19	1	AR067266
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C	51	14.8	1.5	19	1	AR490936
C	52	14.8	1.5	19	1	AX710207
C	53	14.8	1.5	20	1	AR169315
C	54	14.8	1.5	20	1	AR073718
C	55	14.8	1.5	20	1	AR136233
C	56	14.8	1.5	20	1	AR152272
C	57	14.8	1.5	20	1	AR152764
C	58	14.8	1.5	20	1	AR169233
C	59	14.8	1.5	20	1	AR169315
C	60	14.8	1.5	20	1	BD134188
C	61	14.8	1.5	20	1	BD134220
C	62	14.8	1.5	20	1	BD247708
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C	64	14.8	1.5	20	1	AR252791
C	65	14.8	1.5	20	1	AR255072
C	66	14.8	1.5	20	1	AR271128
C	67	14.8	1.5	20	1	AR337123
C	68	14.8	1.5	20	1	AR567361
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C	70	14.8	1.5	20	1	AR567540
C	71	14.8	1.5	20	1	AX139111
C	72	14.8	1.5	20	1	AX402356
C	73	14.8	1.5	20	1	BD014553
C	74	14.8	1.5	21	1	Q0830934
C	75	14.4	1.5	16	1	BD087781
C	76	14.4	1.5	16	1	BD089447
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C	82	14.4	1.5	17	1	AR463914
C	83	14.4	1.5	17	1	AR463917
C	84	14.4	1.5	17	1	AR464028
C	85	14.4	1.5	17	1	AR464039
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C	87	14.4	1.5	17	1	AX227270
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C	89	14.4	1.5	17	1	AX532304
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C	91	14.4	1.5	17	1	AX672211
C	92	14.4	1.5	17	1	AX724315
C	93	14.4	1.5	17	1	AX756862
C	94	14.4	1.5	17	1	AX762013
C	95	14.4	1.5	19	1	AX129890
C	96	14.4	1.5	20	1	AR017550
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C	101	14.4	1.5	20	1	AR255070
C	102	14.4	1.5	20	1	AR255071
C	103	14.4	1.5	20	1	AR255084
C	104	14.4	1.5	20	1	AR255085
C	105	14.4	1.5	20	1	AR315546
C	106	14.4	1.5	20	1	AR437316

C 107	1.5	20	1	AR442464	180	1.4	17	1	AX218250
C 108	1.4	20	1	AX113639	181	1.3	17	1	AX22673
C 109	1.4	20	1	AX270837	182	1.3	17	1	AX22719
C 110	1.4	20	1	AR926507	183	1.3	17	1	AX475294
C 111	1.4	20	1	AR226148	184	1.3	17	1	ACCESSION:AR442594
C 112	1.4	20	1	AR292785	185	1.3	17	1	ACCESSION:AX688306
C 113	1.4	20	1	AX018812	186	1.3	17	1	ACCESSION:AX688307
C 114	1.4	20	1	AR529213	187	1.3	17	1	ACCESSION:AX688308
C 115	1.4	20	1	AX362758	188	1.3	17	1	ACCESSION:AX710205
C 116	1.4	20	1	AR1521	189	1.3	17	1	ACCESSION:AX722998
C 117	1.4	20	1	AR57905	190	1.3	17	1	ACCESSION:AX723190
C 118	1.4	20	1	AR020468	191	1.3	17	1	ACCESSION:AX723403
C 119	1.4	20	1	AR158864	192	1.3	17	1	ACCESSION:AX724208
C 120	1.4	20	1	AR158865	193	1.3	17	1	ACCESSION:AX724823
C 121	1.4	20	1	BD137009	194	1.3	17	1	ACCESSION:AX730357
C 122	1.4	20	1	BD174239	195	1.3	17	1	ACCESSION:AX732995
C 123	1.4	20	1	CD764033	196	1.3	17	1	ACCESSION:AX73511
C 124	1.4	20	1	AR225992	197	1.3	17	1	ACCESSION:AX757042
C 125	1.4	20	1	AR235511	198	1.3	17	1	ACCESSION:AX758322
C 126	1.4	20	1	Q764166	199	1.3	17	1	ACCESSION:AX758322
C 127	1.4	20	1	Q764446	200	1.3	17	1	ACCESSION:AX75774
C 128	1.4	20	1	Q776554	201	1.3	17	1	ACCESSION:AX762695
C 129	1.4	20	1	Q876529	202	1.3	17	1	ACCESSION:AX763346
C 130	1.4	20	1	AR225992	203	1.3	17	1	ACCESSION:AX838300
C 131	1.4	20	1	AR261622	204	1.3	17	1	ACCESSION:AR127420
C 132	1.4	20	1	AR303841	205	1.3	17	1	ACCESSION:BD195707
C 133	1.4	20	1	AR311976	206	1.3	17	1	ACCESSION:AR228200
C 134	1.4	20	1	AR312036	207	1.3	17	1	ACCESSION:AR30514
C 135	1.4	20	1	AR312036	208	1.3	17	1	ACCESSION:AR310596
C 136	1.4	20	1	AR311976	209	1.3	17	1	ACCESSION:AR409029
C 137	1.4	20	1	AR311976	210	1.3	17	1	ACCESSION:AR409049
C 138	1.4	20	1	AR311976	211	1.3	17	1	ACCESSION:AR409436
C 139	1.4	20	1	AR371902	212	1.3	17	1	ACCESSION:AX129940
C 140	1.4	20	1	AX099758	213	1.3	17	1	ACCESSION:AX130849
C 141	1.4	20	1	AX134130	214	1.3	17	1	ACCESSION:AX132384
C 142	1.4	20	1	AX189739	215	1.3	17	1	ACCESSION:BD266374
C 143	1.4	20	1	AX292977	216	1.3	17	1	ACCESSION:AR045661
C 144	1.4	20	1	AR311468	217	1.3	17	1	ACCESSION:Q615745
C 145	1.4	20	1	AR370194	218	1.3	17	1	ACCESSION:AR129940
C 146	1.4	20	1	AR311976	219	1.3	17	1	ACCESSION:Q622855
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C 149	1.4	20	1	AB068830	222	1.3	17	1	ACCESSION:AR192218
C 150	1.4	20	1	AR50451	223	1.3	17	1	ACCESSION:AR192219
C 151	1.4	20	1	AX766430	224	1.3	17	1	ACCESSION:AR12582
C 152	1.4	20	1	AX766434	225	1.3	17	1	ACCESSION:AR211617
C 153	1.4	20	1	AX766434	226	1.3	17	1	ACCESSION:AR325937
C 154	1.4	20	1	Q622850	227	1.3	17	1	ACCESSION:AR326089
C 155	1.4	20	1	Q622850	228	1.3	17	1	ACCESSION:AR326090
C 156	1.4	20	1	Q622849	229	1.3	17	1	ACCESSION:AR326451
C 157	1.4	20	1	Q622849	230	1.3	17	1	ACCESSION:AR40932
C 158	1.4	20	1	Q622850	231	1.3	17	1	ACCESSION:AR456808
C 159	1.4	20	1	Q622850	232	1.3	17	1	ACCESSION:AR456809
C 160	1.4	20	1	Q622854	233	1.3	17	1	ACCESSION:AR456810
C 161	1.4	20	1	Q622854	234	1.3	17	1	ACCESSION:AX183741
C 162	1.4	20	1	AR463912	235	1.3	17	1	ACCESSION:AX218077
C 163	1.4	20	1	AR464026	236	1.3	17	1	ACCESSION:AX227269
C 164	1.4	20	1	AR310832	237	1.3	17	1	ACCESSION:AX475295
C 165	1.4	20	1	BD241277	238	1.3	17	1	ACCESSION:AX475296
C 166	1.4	20	1	Q615747	239	1.3	17	1	ACCESSION:AX53303
C 167	1.4	20	1	Q622847	240	1.3	17	1	ACCESSION:AX532309
C 168	1.4	20	1	Q622848	241	1.3	17	1	ACCESSION:AX5622967
C 169	1.4	20	1	BD227907	242	1.3	17	1	ACCESSION:AX724133
C 170	1.4	20	1	Q622850	243	1.3	17	1	ACCESSION:AX724228
C 171	1.4	20	1	AR196563	244	1.3	17	1	ACCESSION:AX725569
C 172	1.4	20	1	AR328770	245	1.3	17	1	ACCESSION:AX731973
C 173	1.4	20	1	AR456610	246	1.3	17	1	ACCESSION:AX732048
C 174	1.4	20	1	AR463910	247	1.3	17	1	ACCESSION:AX733270
C 175	1.4	20	1	AR463911	248	1.3	17	1	ACCESSION:AX738184
C 176	1.4	20	1	AR461031	249	1.3	17	1	ACCESSION:AX757681
C 177	1.4	20	1	AR461031	250	1.3	17	1	ACCESSION:AX758075
C 178	1.4	20	1	AR482778	251	1.3	17	1	ACCESSION:AX760231
C 179	1.4	20	1	AX218249	252	1.3	17	1	ACCESSION:AX761573

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	c	256	13.4	1.4	18	1	AR297751	c	327
	c	257	13.4	1.4	18	1	AX837998	c	328
	c	258	13.4	1.4	18	1	AX838137	c	329
	c	259	13.4	1.4	19	1	AR004645	c	330
	c	260	13.4	1.4	19	1	ACCBSESSION:AR034557	c	331
	c	261	13.4	1.4	19	1	ACCBSESSION:I89247	c	332
	c	262	13.4	1.4	19	1	ACCBSESSION:AR364420	c	333
	c	263	13.4	1.4	19	1	ACCBSESSION:AX15354	c	334
	c	264	13.4	1.4	19	1	ACCBSESSION:AR04353	c	335
	c	270	13.2	1.4	18	1	ACCBSESSION:AR062299	c	336
	c	271	13.2	1.4	18	1	ACCBSESSION:AX134135	c	337
	c	265	13.4	1.4	19	1	ACCBSESSION:AX189744	c	338
	c	266	13.4	1.4	19	1	ACCBSESSION:AX615126	c	339
	c	267	13.4	1.4	18	1	ACCBSESSION:AR6926	c	340
	c	268	13.2	1.4	18	1	ACCBSESSION:AR9440	c	341
	c	269	13.2	1.4	18	1	ACCBSESSION:BD185912	c	342
	c	270	13.2	1.4	18	1	ACCBSESSION:AR04353	c	343
	c	271	13.2	1.4	18	1	ACCBSESSION:AR062299	c	344
	c	272	13.2	1.4	18	1	ACCBSESSION:AR096626	c	345
	c	273	13.2	1.4	18	1	ACCBSESSION:AR09794	c	346
	c	274	13.2	1.4	18	1	ACCBSESSION:AR13025	c	347
	c	275	13.2	1.4	18	1	ACCBSESSION:BD185912	c	348
	c	276	13.2	1.4	18	1	ACCBSESSION:AR18921	c	349
	c	277	13.2	1.4	18	1	ACCBSESSION:BD250587	c	350
	c	278	13.2	1.4	18	1	ACCBSESSION:168997	c	351
	c	279	13.2	1.4	18	1	ACCBSESSION:I72012	c	352
	c	280	13.2	1.4	18	1	ACCBSESSION:I75091	c	353
	c	281	13.2	1.4	18	1	ACCBSESSION:AR211740	c	354
	c	282	13.2	1.4	18	1	ACCBSESSION:AR215589	c	355
	c	283	13.2	1.4	18	1	ACCBSESSION:AR232057	c	356
	c	284	13.2	1.4	18	1	ACCBSESSION:AR251595	c	357
	c	285	13.2	1.4	18	1	ACCBSESSION:AR281361	c	358
	c	286	13.2	1.4	18	1	ACCBSESSION:AR294630	c	359
	c	287	13.2	1.4	18	1	ACCBSESSION:AR364838	c	360
	c	288	13.2	1.4	18	1	ACCBSESSION:AR48428	c	361
	c	289	13.2	1.4	18	1	ACCBSESSION:AR175950	c	362
	c	290	13.2	1.4	18	1	ACCBSESSION:AX631798	c	363
	c	291	13.2	1.4	18	1	ACCBSESSION:AX696650	c	364
	c	292	13.2	1.4	18	1	ACCBSESSION:AX769496	c	365
	c	293	13.2	1.4	18	1	ACCBSESSION:BD066953	c	366
	c	294	13.2	1.4	18	1	ACCBSESSION:BD085546	c	367
	c	295	13.2	1.4	18	1	ACCBSESSION:BD103977	c	368
	c	296	13.2	1.4	18	1	ACCBSESSION:Y13334	c	369
	c	297	13.2	1.3	13	1	ACCBSESSION:E32325	c	370
	c	298	13.2	1.3	16	1	ACCBSESSION:AR08624	c	371
	c	299	13.2	1.3	16	1	ACCBSESSION:AR305474	c	372
	c	300	13.2	1.3	16	1	ACCBSESSION:AR309578	c	373
	c	301	13.2	1.3	16	1	ACCBSESSION:BD10385	c	374
	c	302	13.2	1.3	17	1	ACCBSESSION:AR046663	c	375
	c	303	13.2	1.3	17	1	ACCBSESSION:AR046710	c	376
	c	304	13.2	1.3	17	1	ACCBSESSION:AR046712	c	377
	c	305	13.2	1.3	17	1	ACCBSESSION:BD241434	c	378
	c	306	13.2	1.3	17	1	ACCBSESSION:Q622962	c	379
	c	307	13.2	1.3	17	1	ACCBSESSION:152715	c	380
	c	308	13.2	1.3	17	1	ACCBSESSION:AX226911	c	381
	c	309	13.2	1.3	17	1	ACCBSESSION:AX59783	c	382
	c	310	13.2	1.3	17	1	ACCBSESSION:AX73310	c	383
	c	311	13.2	1.3	17	1	ACCBSESSION:AR464025	c	384
	c	312	13.2	1.3	17	1	ACCBSESSION:AR8935	c	385
	c	313	13.2	1.3	17	1	ACCBSESSION:AX226910	c	386
	c	314	13.2	1.3	17	1	ACCBSESSION:AX759640	c	387
	c	315	13.2	1.3	17	1	ACCBSESSION:AX769264	c	388
	c	316	13.2	1.3	17	1	ACCBSESSION:AX77824	c	389
	c	317	13.2	1.3	17	1	ACCBSESSION:BD104973	c	390
	c	318	13.2	1.3	17	1	ACCBSESSION:A21773	c	391
	c	319	13.2	1.3	17	1	ACCBSESSION:Q851871	c	392
	c	320	13.2	1.3	17	1	ACCBSESSION:Q858610	c	393
	c	321	13.2	1.3	17	1	ACCBSESSION:AX77824	c	394
	c	322	13.2	1.3	18	1	ACCBSESSION:BD104973	c	395
	c	323	12.8	1.3	16	1	ACCBSESSION:A21773	c	396
	c	324	12.8	1.3	16	1	ACCBSESSION:Q858610	c	397
	c	325	12.8	1.3	16	1	ACCBSESSION:Q858610	c	398

C 399	12.8	1.3	17	1	AX762542	472	1.3	17	1	AR186361	
C 400	12.8	1.3	17	1	AX783962	C 473	12.4	1.3	17	1	ACCESSION: AR190365
C 401	12.8	1.3	17	1	AX783963	C 474	12.4	1.3	17	1	ACCESSION: AR190366
C 402	12.8	1.3	17	1	BD105092	C 475	12.4	1.3	17	1	ACCESSION: AR186006
C 403	12.8	1.3	18	1	AR054591	C 476	12.4	1.3	17	1	ACCESSION: AR302289
C 404	12.8	1.3	18	1	AR066819	C 477	12.4	1.3	17	1	ACCESSION: AR312992
C 405	12.8	1.3	18	1	AR098792	C 478	12.4	1.3	17	1	ACCESSION: AR325310
C 406	12.8	1.3	18	1	BD235033	C 479	12.4	1.3	17	1	ACCESSION: AR125311
C 407	12.8	1.3	18	1	AR292331	C 480	12.4	1.3	17	1	ACCESSION: AR197996
C 408	12.8	1.3	18	1	AR351484	C 481	12.4	1.3	17	1	ACCESSION: AR102479
C 409	12.8	1.3	18	1	AR353630	C 482	12.4	1.3	17	1	ACCESSION: AR134349
C 410	12.8	1.3	18	1	AR481871	C 483	12.4	1.3	17	1	ACCESSION: AR134350
C 411	12.8	1.3	18	1	AX009104	C 484	12.4	1.3	17	1	ACCESSION: AR134351
C 412	12.8	1.3	18	1	AX104436	C 485	12.4	1.3	17	1	ACCESSION: AR134352
C 413	12.8	1.3	18	1	AX104470	C 486	12.4	1.3	17	1	ACCESSION: AR134440
C 414	12.8	1.3	18	1	AX355440	C 487	12.4	1.3	17	1	ACCESSION: AR134441
C 415	12.8	1.3	18	1	AX355441	C 488	12.4	1.3	17	1	ACCESSION: AR134442
C 416	12.8	1.3	18	1	AX412171	C 489	12.4	1.3	17	1	ACCESSION: AR134443
C 417	12.8	1.3	18	1	AX541489	C 490	12.4	1.3	17	1	ACCESSION: AR156907
C 418	12.8	1.3	18	1	AX5417523	C 491	12.4	1.3	17	1	ACCESSION: AR161919
C 419	12.8	1.3	18	1	AX599327	C 492	12.4	1.3	17	1	ACCESSION: AR164636
C 420	12.8	1.3	18	1	AX661825	C 493	12.4	1.3	17	1	ACCESSION: AR164637
C 421	12.8	1.3	18	1	AX708197	C 494	12.4	1.3	17	1	ACCESSION: AR164638
C 422	12.8	1.3	18	1	AX822219	C 495	12.4	1.3	17	1	ACCESSION: AR164639
C 423	12.8	1.3	18	1	AX822859	C 496	12.4	1.3	17	1	ACCESSION: AR182825
C 424	12.8	1.3	17	1	BD186577	C 497	12.4	1.3	17	1	ACCESSION: AX139251
C 425	12.6	1.3	19	1	AX710207	C 498	12.4	1.3	17	1	ACCESSION: AX217682
C 426	12.4	1.3	14	1	AR056994	C 499	12.4	1.3	17	1	ACCESSION: AX218125
C 427	12.4	1.3	14	1	BD23321	C 500	12.4	1.3	17	1	ACCESSION: AX227181
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C 429	12.4	1.3	14	1	AR407917	C 502	12.4	1.3	17	1	ACCESSION: AX227183
C 430	12.4	1.3	14	1	AR407917	C 503	12.4	1.3	17	1	ACCESSION: AX227184
C 431	12.4	1.3	15	1	AX071875	C 504	12.4	1.3	17	1	ACCESSION: AX23072
C 432	12.4	1.3	15	1	AR055659	C 505	12.4	1.3	17	1	ACCESSION: AX263073
C 433	12.4	1.3	15	1	AR056415	C 506	12.4	1.3	17	1	ACCESSION: AX415297
C 434	12.4	1.3	15	1	AR14173	C 507	12.4	1.3	17	1	ACCESSION: AX527151
C 435	12.4	1.3	15	1	BD233337	C 508	12.4	1.3	17	1	ACCESSION: AX527152
C 436	12.4	1.3	15	1	BD251057	C 509	12.4	1.3	17	1	ACCESSION: AX527153
C 437	12.4	1.3	15	1	AR049497	C 510	12.4	1.3	17	1	ACCESSION: AX527154
C 438	12.4	1.3	15	1	AX007891	C 511	12.4	1.3	17	1	ACCESSION: AX52302
C 439	12.4	1.3	16	1	AR633321	C 512	12.4	1.3	17	1	ACCESSION: AX532110
C 440	12.4	1.3	16	1	BD233337	C 513	12.4	1.3	17	1	ACCESSION: AX578912
C 441	12.4	1.3	16	1	AR328443	C 514	12.4	1.3	17	1	ACCESSION: AX579853
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C 443	12.4	1.3	16	1	AX419963	C 516	12.4	1.3	17	1	ACCESSION: AX645752
C 444	12.4	1.3	17	1	AR5019	C 517	12.4	1.3	17	1	ACCESSION: AX634795
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C 446	12.4	1.3	17	1	AR040297	C 519	12.4	1.3	17	1	ACCESSION: AX634833
C 447	12.4	1.3	17	1	AR046854	C 520	12.4	1.3	17	1	ACCESSION: AX634835
C 448	12.4	1.3	17	1	AR057466	C 521	12.4	1.3	17	1	ACCESSION: AX648355
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C 450	12.4	1.3	17	1	AR057728	C 523	12.4	1.3	17	1	ACCESSION: AX671885
C 451	12.4	1.3	17	1	AR057770	C 524	12.4	1.3	17	1	ACCESSION: AX673535
C 452	12.4	1.3	17	1	AR057789	C 525	12.4	1.3	17	1	ACCESSION: AX673690
C 453	12.4	1.3	17	1	AR057790	C 526	12.4	1.3	17	1	ACCESSION: AX688303
C 454	12.4	1.3	17	1	AR057970	C 527	12.4	1.3	17	1	ACCESSION: AX688304
C 455	12.4	1.3	17	1	AR115224	C 528	12.4	1.3	17	1	ACCESSION: AX688466
C 456	12.4	1.3	17	1	AR115270	C 529	12.4	1.3	17	1	ACCESSION: AX688467
C 457	12.4	1.3	17	1	BD241324	C 530	12.4	1.3	17	1	ACCESSION: AX688468
C 458	12.4	1.3	17	1	BD259173	C 531	12.4	1.3	17	1	ACCESSION: AX725790
C 459	12.4	1.3	17	1	Q061547	C 532	12.4	1.3	17	1	ACCESSION: AX726362
C 460	12.4	1.3	17	1	BD13921	C 533	12.4	1.3	17	1	ACCESSION: AX727345
C 461	12.4	1.3	17	1	BD203414	C 534	12.4	1.3	17	1	ACCESSION: AX728438
C 462	12.4	1.3	17	1	AR115486	C 535	12.4	1.3	17	1	ACCESSION: AX729385
C 463	12.4	1.3	17	1	AR115528	C 536	12.4	1.3	17	1	ACCESSION: AX729677
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C 465	12.4	1.3	17	1	AR115548	C 538	12.4	1.3	17	1	ACCESSION: AX73094
C 466	12.4	1.3	17	1	BD13921	C 539	12.4	1.3	17	1	ACCESSION: AX724140
C 467	12.4	1.3	17	1	Q0624573	C 540	12.4	1.3	17	1	ACCESSION: AX724916
C 468	12.4	1.3	17	1	Q0624575	C 541	12.4	1.3	17	1	ACCESSION: AX725258
C 469	12.4	1.3	17	1	Q0624576	C 542	12.4	1.3	17	1	ACCESSION: AX725790
C 470	12.4	1.3	17	1	Q13906	C 543	12.4	1.3	17	1	ACCESSION: AX730652
C 471	12.4	1.3	17	1	Q173170	C 544	12.4	1.3	17	1	ACCESSION: AX731932

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546	12.4	1.3	AX733857	ACCESSION:AX733857	17	1.3	619	12.2	1.3	17	1.3	CQ774981
c 547	12.4	1.3	AX735317	ACCESSION:AX735317	17	1.3	620	12.2	1.3	17	1.3	CQ779633
548	12.4	1.3	AX735539	ACCESSION:AX735539	17	1.3	621	12.2	1.3	17	1.3	ACCESSION:127377
549	12.4	1.3	AX736300	ACCESSION:AX736300	17	1.3	622	12.2	1.3	17	1.3	ACCESSION:134602
550	12.4	1.3	AX736313	ACCESSION:AX736313	17	1.3	623	12.2	1.3	17	1.3	ACCESSION:137605
551	12.4	1.3	AX738273	ACCESSION:AX738273	17	1.3	c 624	12.2	1.3	17	1.3	ACCESSION:152989
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c 556	12.4	1.3	AX756942	ACCESSION:AX756942	17	1.3	c 628	12.2	1.3	17	1.3	ACCESSION:19189988
c 556	12.4	1.3	BD013535	ACCESSION:BD013535	17	1.3	c 634	12.2	1.3	17	1.3	ACCESSION:19190517
c 557	12.4	1.3	BD061979	ACCESSION:BD061979	17	1.3	c 635	12.2	1.3	17	1.3	ACCESSION:19192077
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c 559	12.2	1.3	A04032	ACCESSION:A04032	17	1.3	c 637	12.2	1.3	17	1.3	ACCESSION:19192624
c 560	12.2	1.3	AX760640	ACCESSION:AX760640	17	1.3	c 638	12.2	1.3	17	1.3	ACCESSION:19286516
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c 565	12.2	1.3	A07276	ACCESSION:A07276	17	1.3	c 643	12.2	1.3	17	1.3	ACCESSION:19286429
c 566	12.2	1.3	A14911	ACCESSION:A14911	17	1.3	c 644	12.2	1.3	17	1.3	ACCESSION:19286516
c 567	12.2	1.3	A30566	ACCESSION:A30566	17	1.3	c 645	12.2	1.3	17	1.3	ACCESSION:19322012
c 568	12.2	1.3	A34171	ACCESSION:A34171	17	1.3	c 646	12.2	1.3	17	1.3	ACCESSION:19324984
c 569	12.2	1.3	A34558	ACCESSION:A34558	17	1.3	c 647	12.2	1.3	17	1.3	ACCESSION:19325440
c 570	12.2	1.3	A66925	ACCESSION:A66925	17	1.3	c 648	12.2	1.3	17	1.3	ACCESSION:19325919
c 571	12.2	1.3	A69925	ACCESSION:A69925	17	1.3	c 649	12.2	1.3	17	1.3	ACCESSION:19325948
c 572	12.2	1.3	A75920	ACCESSION:A75920	17	1.3	c 650	12.2	1.3	17	1.3	ACCESSION:19326493
c 573	12.2	1.3	A14911	ACCESSION:A14911	17	1.3	c 651	12.2	1.3	17	1.3	ACCESSION:19328006
c 574	12.2	1.3	A30566	ACCESSION:A30566	17	1.3	c 652	12.2	1.3	17	1.3	ACCESSION:19328214
c 575	12.2	1.3	A43171	ACCESSION:A43171	17	1.3	c 653	12.2	1.3	17	1.3	ACCESSION:19328215
c 576	12.2	1.3	A46572	ACCESSION:A46572	17	1.3	c 654	12.2	1.3	17	1.3	ACCESSION:19328217
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c 589	12.2	1.3	BD20794	ACCESSION:BD0794	17	1.3	c 667	12.2	1.3	17	1.3	ACCESSION:19456772
c 590	12.2	1.3	BD203339	ACCESSION:BD203339	17	1.3	c 668	12.2	1.3	17	1.3	ACCESSION:19456773
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c 603	12.2	1.3	BD2515709	ACCESSION:BD2515709	17	1.3	c 681	12.2	1.3	17	1.3	ACCESSION:19464988
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c 617	12.2	1.3	BD2623923	ACCESSION:BD2623923	17	1.3	c 695	12.2	1.3	17	1.3	ACCESSION:19465024
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TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1369

RESULT 99
Query Match 1.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 14; Conservative 0; Mismatches 0; Indels 0

QV 436 AAACCAAAGACCCC 449
Db 18 AAACCAAAGACCCC 5

Sequence 728, Application US/08679645
Patient No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwigan, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Shokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 728:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-728

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Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 49 CTCCCCACCAAGAAAGA 65
Db 17 CTCACCAACAAACA 1

RESULT 1.00
US-09-371-772B-6172
; Sequence 6172, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ridozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigan, Jim
; APPLICANT: Steincomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBB001-876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6172
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6172

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 269 GAAATAAGAACATGGAGCC 285
Db 1. GAAAUAGACACUGGAGCC 17

RESULT 1.01
US-09-366-108A-487
; Sequence 487, Application US/09866108A
; Patent No. 6685188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEGOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 487
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-487

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 159 AACCCAGAGGAAGTGC 175
Db 1 AACTGAGGAAGTGC 17

RESULT 103
US-09-866-108A-7588
; Sequence 7589, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenshang
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; FILE REFERENCE: AEMICIA-7
; CURRENT FILING DATE: 2001-05-25
; CURRENT FILING NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7588
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7588

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 160 ACCCAGAGGAAGTGC 176
Db 1 ACTGAGGAAGTGC 17

RESULT 104
US-09-866-108A-7707/c
; Sequence 7707, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7587
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7587

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GenCore version 5.1.6									
Copyright (c) 1993 - 2005 Compugen Ltd.									
4 nucleic - nucleic search, using sw model									
run on: June 27, 2005, 17:01:05 ; Search time 6 Seconds (without alignments) 4.283 Million cell updates/sec									
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7	20	2.1	20	1	US-09-915-814-22	Sequence 22, App1			
8	20	2.1	20	1	US-09-915-814-23	Sequence 23, App1			
9	20	2.1	20	1	US-09-915-814-24	Sequence 24, App1			
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13	20	2.1	20	1	US-09-915-814-28	Sequence 28, App1			
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16	20	2.1	20	1	US-09-915-814-31	Sequence 31, App1			
17	20	2.1	20	1	US-09-915-814-32	Sequence 32, App1			
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21	18.6	1.9	25	1	US-10-719-900-78028	Sequence 78028,			
22	18.6	1.9	25	1	US-10-719-900-901836	Sequence 901836,			
23	18.4	1.9	21	1	US-10-786-720-8187	Sequence 8187, App			
24	18.4	1.9	21	1	US-10-786-720-10419	Sequence 10419, A			
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27	18.4	1.9	25	1	US-10-809-189-81464	Sequence 81464, A			
28	18.2	1.9	25	1	US-09-866-108-12485	Sequence 12485, A			
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c 115	1.6	US-10-479-670-215	Sequence 215, APP
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c 136	1.5	US-09-863-806-12	Sequence 12, APP
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c 141	1.5	US-10-001-863-25	Sequence 25, APP
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c 143	1.5	US-10-290-473-12	Sequence 12, APP
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c 148	1.5	US-10-216-544-84	Sequence 84, APP
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c 151	1.5	US-10-316-745A-8	Sequence 8, APP
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c 154	1.5	US-10-915-557-5	Sequence 5, APP
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c 158	1.5	US-10-917-330-44	Sequence 44, APP
c 159	1.5	US-10-831-901A-8346	Sequence 8346, APP
c 160	1.5	US-10-831-901A-8347	Sequence 8347, APP
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c 163	1.5	US-10-786-720-11108	Sequence 1108, APP
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c 165	1.5	US-09-866-108-7594	Sequence 7594, APP
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c 169	1.5	US-10-947-938-456	Sequence 456, APP
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c 172	1.5	US-09-866-108-7594	Sequence 7594, APP
c 173	1.5	US-09-866-108-7594	Sequence 7594, APP
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c 175	1.5	US-09-780-664-424	Sequence 424, APP
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c 180	14.4	US-10-723-361-7705	Sequence 7705, APP
c 181	14.4	US-09-537-2405	Sequence 2805, APP
c 182	14.4	US-10-606-133-245	Sequence 215, APP
c 183	14.4	US-09-796-599-3	Sequence 3, APP
c 184	14.4	US-09-957-837A-12	Sequence 12, APP
c 185	14.4	US-09-957-837A-12	Sequence 146, APP
c 186	14.4	US-09-957-837A-12	Sequence 146, APP
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c 189	14.4	US-10-062-651-19	Sequence 19, APP
c 190	14.4	US-10-062-920-19	Sequence 19, APP
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c 194	14.4	US-10-062-624-19	Sequence 355, APP
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c 196	14.4	US-10-241-780-359	Sequence 369, APP
c 197	14.4	US-10-448-836-72	Sequence 72, APP
c 198	14.4	US-10-160-807-168	Sequence 168, APP
c 199	14.4	US-10-159-605-70	Sequence 10, APP
c 200	14.4	US-10-159-956-124	Sequence 124, APP
c 201	14.4	US-10-448-944-72	Sequence 72, APP
c 202	14.4	US-10-185-057-15	Sequence 47, APP
c 203	14.4	US-10-185-057-23	Sequence 41, APP
c 204	14.4	US-10-188-470-21	Sequence 23, APP
c 205	14.4	US-10-159-947-618	Sequence 19, APP
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c 213	14.4	US-10-492-928A-64	Sequence 143, APP
c 214	14.4	US-10-954-723A-12	Sequence 4520, APP
c 215	14.4	US-09-969-733-496	Sequence 2496, APP
c 216	14.2	US-10-25-02-2811	Sequence 281, APP
c 217	14.2	US-09-978-192A-21	Sequence 21, APP
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c 229	14.2	US-09-978-193A-21	Sequence 21, APP
c 230	14.2	US-09-978-193A-21	Sequence 21, APP
c 231	14.2	US-09-978-197-29	Sequence 29, APP
c 232	14.2	US-09-978-187-487	Sequence 487, APP
c 233	14.2	US-09-99-333A-21	Sequence 21, APP
c 234	14.2	US-09-978-193A-21	Sequence 21, APP
c 235	14.2	US-09-978-193A-21	Sequence 21, APP
c 236	14.2	US-09-978-824-21	Sequence 21, APP
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c 238	14.2	US-09-978-585A-21	Sequence 21, APP
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c 243	14.2	US-09-978-197-29	Sequence 29, APP
c 244	14.2	US-09-978-187-487	Sequence 487, APP
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c 246	14.2	US-09-978-175A-21	Sequence 21, APP
c 247	14.2	US-09-978-298A-21	Sequence 21, APP
c 248	14.2	US-09-978-188A-21	Sequence 21, APP
c 249	14.2	US-09-978-281A-21	Sequence 21, APP
c 250	14.2	US-09-978-194A-21	Sequence 21, APP
c 251	14.2	US-09-978-299A-21	Sequence 21, APP
c 252	14.2	US-09-978-299A-21	Sequence 21, APP

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c 112	20	0.8	Sequence 148, App	15.4	0.6	Sequence 22, Appli	19	1	US-10-441-925A-22
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c 119	20	0.8	Sequence 155, App	15.4	0.6	Sequence 3583, App	17	1	US-10-61-155-3583
c 120	20	0.8	Sequence 156, App	15.4	0.6	Sequence 1479, App	17	1	US-10-061-201-1479
c 121	20	0.8	Sequence 157, App	15.4	0.6	Sequence 1480, App	17	1	US-10-061-201-1480
c 122	20	0.8	Sequence 158, App	15.4	0.6	Sequence 3582, App	17	1	US-10-209-787-3582
c 123	20	0.8	Sequence 159, App	15.4	0.6	Sequence 3583, App	17	1	US-10-209-787-3583
c 124	20	0.8	Sequence 160, App	15.4	0.6	Sequence 3582, App	17	1	US-10-261-185-3582
c 125	20	0.8	Sequence 161, App	15.4	0.6	Sequence 3583, App	17	1	US-10-61-155-3583
c 126	20	0.8	Sequence 162, App	15.4	0.6	Sequence 1531, App	17	1	US-10-723-361-1531
c 127	20	0.8	Sequence 163, App	15.4	0.6	Sequence 1532, App	17	1	US-10-723-361-1532
c 128	20	0.8	Sequence 164, App	15.4	0.6	Sequence 1533, App	17	1	US-10-723-361-1533
c 129	20	0.8	Sequence 165, App	15.4	0.6	Sequence 3582, App	17	1	US-10-681-074-3582
c 130	20	0.8	Sequence 166, App	15.4	0.6	Sequence 3583, App	17	1	US-10-681-074-3583
c 131	20	0.8	Sequence 167, App	15.4	0.6	Sequence 50, Appli	17	1	US-10-961-077-1169
c 132	20	0.8	Sequence 168, App	15.4	0.6	Sequence 1169, App	17	1	US-10-961-077-1169
c 133	20	0.8	Sequence 169, App	15.4	0.6	Sequence 130, App	17	1	US-10-398-308-130
c 134	20	0.8	Sequence 170, App	15.4	0.6	Sequence 9, Appli	17	1	US-10-227-719D-9
c 135	19	0.7	Sequence 171, App	15.4	0.6	Sequence 17, Appli	17	1	US-10-283-881-17
c 136	19	0.7	Sequence 172, App	15.4	0.6	Sequence 5, Appli	17	1	US-10-295-903-5
c 137	18	0.7	Sequence 173, App	15.4	0.6	Sequence 16, App	17	1	US-10-178-325-161
c 138	18	0.7	Sequence 174, App	15.4	0.6	Sequence 19, Appli	17	1	US-09-91-314-19
c 139	18	0.7	Sequence 175, App	15.4	0.6	Sequence 9, Appli	17	1	US-09-829-155C-9
c 140	18	0.7	Sequence 176, App	15.4	0.6	Sequence 15, Appli	17	1	US-09-943-388-15
c 141	19	0.7	Sequence 177, App	15.4	0.6	Sequence 21, Appli	17	1	US-09-97-365-21
c 136	19	0.7	Sequence 178, App	15.4	0.6	Sequence 1450, App	17	1	US-10-712-672-1490
c 137	18	0.7	Sequence 179, App	15.4	0.6	Sequence 558, App	17	1	US-09-877-478-117
c 138	18	0.7	Sequence 180, App	15.4	0.6	Sequence 806, App	17	1	US-09-866-108-558
c 139	18	0.7	Sequence 181, App	15.4	0.6	Sequence 1336, App	17	1	US-09-848-754A-1396
c 140	18	0.7	Sequence 182, App	15.4	0.6	Sequence 2630, App	17	1	US-09-866-108-2630
c 141	19	0.7	Sequence 183, App	15.4	0.6	Sequence 2672, App	17	1	US-09-866-108-2672
c 136	19	0.7	Sequence 184, App	15.4	0.6	Sequence 2673, App	17	1	US-09-97-365-21
c 137	18	0.7	Sequence 185, App	15.4	0.6	Sequence 1117, App	17	1	US-09-740-332-2938
c 138	18	0.7	Sequence 186, App	15.4	0.6	Sequence 2939, App	17	1	US-09-740-332-2939
c 139	18	0.7	Sequence 187, App	15.4	0.6	Sequence 367, App	17	1	US-09-792-818-367
c 140	18	0.7	Sequence 188, App	15.4	0.6	Sequence 7, Appli	17	1	US-09-848-754A-3089
c 141	19	0.7	Sequence 189, App	15.4	0.6	Sequence 3089, App	17	1	US-09-848-754A-3089
c 136	19	0.7	Sequence 190, App	15.4	0.6	Sequence 3091, App	17	1	US-09-740-332-1214
c 142	17	0.8	Sequence 191, App	15.4	0.6	Sequence 1214, App	17	1	US-09-877-478-117
c 143	17	0.8	Sequence 192, App	15.4	0.6	Sequence 2938, App	17	1	US-09-877-478-117
c 144	17	0.7	Sequence 193, App	15.4	0.6	Sequence 2939, App	17	1	US-09-740-332-2938
c 145	17	0.6	Sequence 194, App	15.4	0.6	Sequence 1117, App	17	1	US-09-342-902-117
c 146	16	0.8	Sequence 195, App	15.4	0.6	Sequence 806, App	17	1	US-09-855-612-7
c 147	16	0.8	Sequence 196, App	15.4	0.6	Sequence 1214, App	17	1	US-09-817-879-1214
c 148	16	0.8	Sequence 197, App	15.4	0.6	Sequence 2938, App	17	1	US-09-740-332-1214
c 149	16	0.8	Sequence 198, App	15.4	0.6	Sequence 1214, App	17	1	US-09-817-879-1214
c 150	16	0.8	Sequence 199, App	15.4	0.6	Sequence 2938, App	17	1	US-09-817-879-1214
c 151	16	0.8	Sequence 200, App	15.4	0.6	Sequence 1117, App	17	1	US-09-342-902-117
c 152	16	0.8	Sequence 201, App	15.4	0.6	Sequence 3518, App	17	1	US-09-848-754A-3089
c 153	16	0.8	Sequence 202, App	15.4	0.6	Sequence 1477, App	17	1	US-09-927-046-1165
c 154	16	0.8	Sequence 203, App	15.4	0.6	Sequence 2110, App	17	1	US-09-927-046-1165
c 155	16	0.8	Sequence 204, App	15.4	0.6	Sequence 5857, App	17	1	US-10-156-306-5857
c 156	16	0.8	Sequence 205, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 157	16	0.8	Sequence 206, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 158	16	0.8	Sequence 207, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 159	16	0.8	Sequence 208, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 160	16	0.8	Sequence 209, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 161	16	0.8	Sequence 210, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 162	16	0.8	Sequence 211, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 163	16	0.8	Sequence 212, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 164	16	0.8	Sequence 213, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 165	16	0.6	Sequence 214, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 166	16	0.6	Sequence 215, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 167	16	0.6	Sequence 216, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 168	16	0.6	Sequence 217, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 169	15	0.8	Sequence 218, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 170	15	0.8	Sequence 219, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 171	15	0.8	Sequence 220, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 172	15	0.8	Sequence 221, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 173	15	0.8	Sequence 222, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 174	15	0.8	Sequence 223, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 175	15	0.8	Sequence 224, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 176	15	0.8	Sequence 225, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 177	15	0.8	Sequence 226, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 178	15	0.8	Sequence 227, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 179	15	0.8	Sequence 228, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 180	15	0.8	Sequence 229, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 181	15	0.8	Sequence 230, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 182	15	0.8	Sequence 231, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 183	15	0.8	Sequence 232, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 184	15	0.8	Sequence 233, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 185	15	0.8	Sequence 234, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 186	15	0.8	Sequence 235, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
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c 188	15	0.8	Sequence 237, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 189	15	0.8	Sequence 238, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 190	15	0.8	Sequence 239, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 191	15	0.8	Sequence 240, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 192	15	0.8	Sequence 241, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 193	15	0.8	Sequence 242, App	15.4	0.6	Sequence 2996, App	17	1	US-10-238-700-2996
c 194	15	0.8	Sequence 243, App	15.4	0.6	Sequence 3518, App	17	1	US-10-342-902-806
c 195	15	0.8	Sequence 244, App	15.4	0.6	Sequence 1477, App	17	1	US-10-321-039-541
c 196	15	0.8	Sequence 245, App	15.4	0.6	Sequence 263, App	17	1	US-09-866-108-556
c 197	15	0.8	Sequence 246, App	15.4	0.6	Sequence 452, App	17	1	US-10-156-306-5857
c 198	15	0.8	Sequence 247, App	15.4	0.6	Sequence 5980, App	17	1	US-10-156-306-5857
c 199	15	0.8							

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: * June 27, 2005, 16:51:28 ; Search time 0.001 Seconds

(without alignment) 296.820 Million cell updates/sec

Title: us-09-915-814-3
 Perfect score: 970

Sequence: 1 cttctgttaaagaggatcata.....tttcttagtgggtcgatgat 970

Scoring table: IDENTITY_NUC Gapext 0.5

Searched: 10 seqs, 153 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 10 summaries

Database : rstdb : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	15.2		1.6	21	1	TA181D04Q	ACCESSION: AI474441
c 2	13.8		1.4	19	1	CL680274	ACCESSION: CL680274
c 3	12		1.2	12	1	CL432297	ACCESSION: CL432297
c 4	11.4		1.2	14	1	CL688513	ACCESSION: CL688513
c 5	11.4		1.2	16	1	BG897738	ACCESSION: BG897738
c 6	11.2		1.2	16	1	AJ594105	ACCESSION: AJ594105
c 7	10.8		1.1	14	1	AJ688262	ACCESSION: AJ688262
c 8	10.8		1.1	15	1	CL439508	ACCESSION: CL439508
c 9	10.4		1.1	13	1	BQ586028	ACCESSION: BQ586028
c 10	10.4		1.1	13	1	CL437480	ACCESSION: CL437480

ALIGNMENTS

TA181D04Q/c

DEFINITION T. brucei sheared genomic DNA clone 181d04, reverse sequence, genomic survey sequence.

ACCESSION AL474441

VERSION AL474441.1

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatida;

Trypanosoma brucei

Hall.N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

REFERENCE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

Query Match 1.4% ; Score 13.8 ; DB 1 ; Length 19 ;

Best Local Similarity 88.2% ; Pred. No. 1.1 ;

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrel@barrell@sanger.ac.uk and nhil@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (~ 4 kb). The v+ is method used for the library construction is described in detail in Smith, H. and Ventur, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In: Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: neilsay@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers

source 1..21

/organism="Trypanosoma brucei"

/mol type="Genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="181d04"

/

Query Match 1.6% ; Score 15.2 ; DB 1 ; Length 21 ;

Best Local Similarity 85.0% ; Pred. No. 0.59 ;

Matches 17 ; Conservative 0 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 823 ACAGTCAGACAGCAACAA 842

Db 21 ACAGACACACACACACAA 2

RESULT 2

CL680274/c

LOCUS PRI0128c_E09_2 - PRI0128c.BR (19) Note: Recurring String Mixed

DEFINITION stage foenid -library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL680274

VERSION CL680274.1

KEYWORDS GSS.

SOURCE Pristionchus pacificus

PRISTIONCHUS PACIFICUS

PRISTIONCHUS PACIFICUS

Eukaryota; Metazoa; Nemata; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE AppDB: an AceDB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT Contact: Sommer,RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Email: ralf.sommer@uebingen.mpg.de

This library was generated at Caltach, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: foenid ends.

FEATURES Location/Qualifiers

source 1..19

/organism="Pristionchus pacificus"

/mol type="Genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone lib="Mixed stage fosmid library of P. pacificus

var. California"

/note=Vector: pEPifos-5 Fosmid vector"

Query Match 1.4% ; Score 13.8 ; DB 1 ; Length 19 ;

Best Local Similarity 88.2% ; Pred. No. 1.1 ;

Directional ⁿ									
Query Match	1.2%	Score 11.4;	DB 1;	Length 16;					
Best Local Similarity	92.3%	Pred. No 3.3;							
Matches	12;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	116 AGCTGCCCTAAAA 128								
Db	15 AGCTGCCCTAAAA 3								
RESULT 6									
LOCUS	AJ594105	16 bp	DNA	linear	GSS 15-JAN-2004				
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 392H05, genomic survey sequence.								
ACCESSION	AJ594105								
VERSION	AJ594105.1	GI:37943729							
KEYWORDS	Arabidopsis thaliana (thale cress)								
ORGANISM	Arabidopsis thaliana								
	Bikaryotyta; Streptophytina; Embryophytina; Tracheophyta;								
	Spermatophytina; Magnoliophytina; eu dicotyledons; core eudicots;								
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.								
REFERENCE	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lechat, A.								
AUTHORS									
TITLE	T-DNA insertion into the Arabidopsis genome depends on sequences of pre-insertion sites								
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)								
MEDLINE	22363535								
PUBLMED	12446565								
FEATURES	2 (bases 1 to 16)								
AUTHORS	Balzergue, S.								
TITLE	Direct Submission								
JOURNAL	Submitted (23-OCT-2003) Balzergue S., INRGV, INRA/CNRS, 2 rue Gaston Crémieux, 91075 Evry cedex, FRANCE								
COMMENT	PCR was performed on DNA from transformants of <i>Arabidopsis thaliana</i> plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publicines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.Genoplante.com and http://genoplante-info.infobiogen.fr).								
FEATURES	source								
	1. .16								
	/organism="Arabidopsis thaliana"								
	/mol_type="genomic DNA"								
	/cultivar="Wislilewskija"								
	/db_xref="taxon:3702"								
	/clone="392H06"								
	/clone_lib=Arabidopsis thaliana T-DNA insertion lines"								
	1. .16								
	/note="T-DNA flanking sequence								
	left border"								
Query Match	1.2%	Score 11.2;	DB 1;	Length 16;					
Best Local Similarity	81.2%	Pred. No 3.6;							
Matches	13;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	474 AACATGATGCTGATC 489								
Db	16 AAAATTATGATC 1								
RESULT 7									
LOCUS	AJ688262	14 bp	mRNA	linear	EST 29-JUN-2004				
DEFINITION	AJ688262 KN261 Bos taurus cDNA clone KN261-047_017, mRNA sequence.								
ACCESSION	AJ688262								
VERSION	AJ688262.1	GI:49420852							
KEYWORDS	EST.								
SOURCE	Bos taurus (cow)								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.								
REFERENCE	1 (bases 1 to 14)								
AUTHORS	Anderson, S.I., Finlayson, H.A. and Archibald, A.L.								
TITLE	Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle								
JOURNAL	Unpublished (2004)								
COMMENT	Contact: Anderson, S.I. Genomics and Bioinformatics Roslin Institute, Midlothian, EH25 9PS, UNITED KINGDOM								
	Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the rmisscore 20 and -minmatch 12 options. Vector: pBlueScriptII (SK+). Site1: EcORI R. Site2: SmaI 3', Seq Primer M13F Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkogenomics.org .								
LOCATION/QUALIFIERS	1. .14								
	/organism="Bos taurus"								
	/mol_type="mRNA"								
	/db_xref="taxon:9913"								
	/clone="KN261-047_017"								
	/tissue type="ovary"								
	/clone_id="KN261"								
	/note=Vector: pBlueScriptII (SK+); Site 1: EcORI; Site 2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."								
Query Match	1.1%	Score 10.8;	DB 1;	Length 14;					
Best	Local	Similarity	85.7%	Pred. No. 4.3;					
Matches	12;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	890 GGATTCTAACAA 903								
Db	1 GAAATTCTAAAAAA 14								
RESULT 8									
LOCUS	CL439508	15 bp	DNA	linear	GSS 18-MAR-2004				
DEFINITION	PST9427-NR.Seq MICB1 Mus musculus genomic clone PST9427-NR.Seq, genomic survey sequence.								
ACCESSION	CL439508								
VERSION	CL439508.1	GI:45577088							
KEYWORDS	GSS.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
REFERENCE	1 (bases 1 to 15)								
AUTHORS	Hicks, G.G.								
TITLE	www.3scells.ca								
JOURNAL	Unpublished (2002)								
COMMENT	Contact: Hicks, G.G. Mammalian Functional Genomics Centre, Manitoba Institute of Cell Biology, University of Manitoba, ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada Tel: 204 787 2133 Fax: 204 787 2190 Email: hicksgg@cc.umanitoba.ca								
Query Match	1.2%	Score 11.2;	DB 1;	Length 16;					
Best Local Similarity	81.2%	Pred. No 3.6;							
Matches	13;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	474 AACATGATGCTGATC 489								
Db	16 AAAATTATGATC 1								
RESULT 7									
LOCUS	AJ688262	14 bp	mRNA	linear	EST 29-JUN-2004				

http://140.193.242.7/eddb/public_search_frame.php?PST=PST9427-NR.Se

Class: Gene Trap.

FEATURES

source

Location/Qualifiers

1..15

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129 sv"

/db_xref="taxon:10090"

/clone="PST9427-NR.Seq"

/sex="Male"

/cell_type="Embryonic stem cell"

/cell_line="D3H (J1 subclone)"

/clone_lib="MICB1"

/note="Vector: U3NeoSV1"

Query Match 1.1%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 4.3;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 480 ATGCTGATGCCAG 493

Db 14 ATGCTGAGTCCAG 1

RESULT 9

LOCUS BQ586028 13 bp mRNA linear EST 06-DEC-2002

DEFINITION E012394-024-013-F21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

024-013-P21 5'-PRIME, mRNA sequence.

ACCESSION BQ586028

VERSION BQ586028.1

GI:26115610

KEYWORDS EST.

ORGANISM Beta vulgaris

Beta vulgaris; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amananthaceae; Beta.

REFERENCE 1 (bases 1 to 13).

AUTHORS Herwig,R., Schulz,B., Weissaar,B., Henning,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H., Radefeld,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22426189

PUBMED 12472698

COMMENT Contact: Weissaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linné-Weg 10, 50829 Koele, Germany

Fax: 0049221562851

Email: weissaar@mpiz-koele.mpg.de

Insert length: 13 Std Error: 0.00

Plate: 13 row: F column: 21

Seq primer: SP6; CATACGATTTAGGTGACATATAG.

FEATURES

source

Location/Qualifiers

1..13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:186018"

/clone="024-013-F21"

/tissue_type="leaf"

/lab_host="EMDH10"

/clone_lib="MP12-ADIS-024-leaf"

/note="Vector: PCMVSPORT26: Site 1: SalI: Site 2: NotI: cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzaeh AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-SalI-CCACCGTCCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beta project, local PI: Dr. Katharina Schnieder, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 5.1;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 518 TCTGCTTCACAA 529

Db 2 TCTGCTTAACAA 13

RESULT 10

LOCUS CL437480 13 bp DNA linear GSS 18-MAR-2004

DEFINITION PSITS604-NR.Seq MICB1 Mus musculus genomic clone PST5604-NR.Seq

Similar to BC031107, genomic survey sequence.

ACCESSION CL437480

VERSION CL437480.1 GI:45573210

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 13).

AUTHORS Hicks,G.G.

TITLE www.Escalls.ca

JOURNAL Unpublished (2002)

COMMENT Contact: Hicks GG

Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

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Fax: 204 787 2190

Email: hicks@cc.umanitoba.ca

U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available.

Sequence analysis available from

http://140.193.242.7/eddb/public_search_frame.php?PST=PST5604-NR.Se

Qy 907 TCAGGGACTATC 918

Db 1 TCAGGGAGTAC 12

Query Match 1.1%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 5.1;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 907 TCAGGGACTATC 918

Db 1 TCAGGGAGTAC 12

Search completed: June 27, 2005, 16:51:28

Job time : 0.001 secs